GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:50:52 ; Search time 114 Seconds
(without alignments)
34.688 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	2	AAW99195	Aaw99195 Minor his
2	36	97.3	9	2	AAW99196	Aaw99196 Minor his
3	36	97.3	9	2	AAW99197	Aaw99197 Minor his
4	36	97.3	9	2	AAW97572	Aaw97572 T-cell ep
5	36	97.3	9	2	AAW97375	Aaw97375 HA-1 H-al
6	36	97.3	9	2	AAW97374	Aaw97374 HA-1 R-al
7	36	97.3	9	8	ADH40333	Adh40333 Human min
8	36	97.3	9	8	ADH40334	Adh40334 Human min
9	36	97.3	13	2	AAW99199	Aaw99199 vR cell K
10	36	97.3	13	2	AAW99198	Aaw99198 DH cell K
11	36	97.3	13	2	AAW97415	Aaw97415 KIAA0223
12	36	97.3	13	2	AAW97414	Aaw97414 KIAA0223
13	28	75.7	10	6	ABP71119	Abp71119 E10 prote
14	26	70.3	9	8	ADT73023	Adt73023 Human RSV
15	26	70.3	10	2	AAW73901	Aaw73901 B. forsyt
16	25	67.6	10	4	AAG94234	Aag94234 Human com
17	25	67.6	10	8	ADQ26722	Adq26722 Topo V Hh
18	25	67.6	11	7	ADD23269	Add23269 Breast ca
19	25	67.6	12	2	AAW64577	Aaw64577 Human Fac
20	25	67.6	13	5	ADG66269	Adg66269 Human pro
21	25	67.6	13	5	ADG66272	Adg66272 Human pro
22	25	67.6	13	5	ADG66271	Adg66271 Human pro
23	25	67.6	13	5	ADG66270	Adg66270 Human pro
24	25	67.6	15	5	ABB07889	Abb07889 Phosphoen
25	24	64.9	9	8	ABY01546	Aby01546 SARS coro
26	24	64.9	9	9	ADZ50925	Adz50925 Y. pestis
27	24	64.9	10	6	ABR04849	Abr04849 Human can
28	24	64.9	10	8	ABY01491	Aby01491 SARS coro
29	24	64.9	10	9	ADY49658	Ady49658 Severe ac
30	24	64.9	10	9	AEC01228	Aec01228 SARS vira
31	24	64.9	13	6	AAE34759	Aae34759 Streptomy
32	24	64.9	13	7	ADD23767	Add23767 Breast ca
33	24	64.9	14	7	ADD23419	Add23419 Breast ca
34	24	64.9	15	6	ABR30509	Abr30509 Human can
35	24	64.9	15	6	ABR30940	Abr30940 Human can
36	24	64.9	15	6	ABR31271	Abr31271 Human can
37	24	64.9	15	6	ABR30473	Abr30473 Human can
38	24	64.9	15	6	ABR30612	Abr30612 Human can
39	24	64.9	15	6	ABR31028	Abr31028 Human can
40	24	64.9	15	6	ABR30613	Abr30613 Human can
41	24	64.9	15	6	ABR31170	Abr31170 Human can
42	24	64.9	15	6	ABR30941	Abr30941 Human can
43	24	64.9	15	6	ABR31063	Abr31063 Human can
44	24	64.9	15	6	ABR31169	Abr31169 Human can
45	24	64.9	15	6	ABR31559	Abr31559 Human can

ALIGNMENTS

RESULT 1
AAW99195
ID AAW99195 standard; peptide; 9 AA.
XX
AC AAW99195;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /label= His, Arg
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 1; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the

```
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 2
AAW99196
ID   AAW99196 standard; peptide; 9 AA.
XX
AC   AAW99196;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Claim 3; Page 32; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 3
AAW99197
ID   AAW99197 standard; peptide; 9 AA.
XX
AC   AAW99197;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Disclosure; Page 15; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 4
AAW97572
ID   AAW97572 standard; peptide; 9 AA.
XX
AC   AAW97572;
XX
DT   20-MAY-1999  (first entry)
XX
DE   T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW   T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW   transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW   neoplastic haematopoietic cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /note= "His or Arg"
XX
```

PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Claim 1; Page 39; 57pp; English.
XX
CC The present sequence represents an immunogenic peptide constituting a T-
CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC The peptide can be used in vaccines or pharmaceutical formulations as
CC medicines to induce tolerance for transplants so as to prevent rejection
CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC I context, can be eliminated after specific recognition of the peptides.
CC The peptides can also be used to raise antibodies, T-cell receptor, B-
CC and T-cells
XX
SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||||||||
Db 1 VLXDDLLEA 9

RESULT 5
AAW97375
ID AAW97375 standard; protein; 9 AA.
XX
AC AAW97375;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 H-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 18; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 H-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC anti-idiotypic B cells and/or T cells and antibodies
XX
SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| |||||
Db 1 VLHDDLLEA 9

RESULT 6
AAW97374
ID AAW97374 standard; protein; 9 AA.
XX
AC AAW97374;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 R-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 13; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 R-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used

```
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
ADH40333
ID   ADH40333 standard; peptide; 9 AA.
XX
AC   ADH40333;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 8
ADH40334
ID   ADH40334 standard; peptide; 9 AA.
XX
AC   ADH40334;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 9
AAW99199
ID   AAW99199 standard; peptide; 13 AA.
```

XX
AC AAW99199;
XX
DT 20-MAY-1999 (first entry)
XX
DE vR cell KIAA0223 protein sequence.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Synthetic.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
DR N-PSDB; AAX19409.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 31; 47pp; English.
XX
CC The present invention describes a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases. The present sequence represents a KIAA0223 sequence given in
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 97.3%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 3 VLHDDLLEA 11

RESULT 10
AAW99198
ID AAW99198 standard; peptide; 13 AA.
XX
AC AAW99198;
XX
DT 20-MAY-1999 (first entry)
XX
DE DH cell KIAA0223 protein sequence.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Synthetic.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
DR N-PSDB; AAX19408.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 31; 47pp; English.
XX
CC The present invention describes a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases. The present sequence represents a KIAA0223 sequence given in
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 97.3%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 3 VLRDDLLEA 11

RESULT 11
AAW97415
ID AAW97415 standard; protein; 13 AA.
XX
AC AAW97415;
XX
DT 20-MAY-1999 (first entry)
XX
DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
OS Homo sapiens.
XX
PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
DR N-PSDB; AAX16081.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-

PT versus-host disease.
XX
PS Disclosure; Page 38; 57pp; English.
XX
CC The present sequence represents the KIAA0223 polymorphism in HA-1
CC positive homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or Graft-versus-Host
CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ Sequence 13 AA;

Query Match 97.3%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 3 VLHDDLLEA 11

RESULT 12
AAW97414
ID AAW97414 standard; protein; 13 AA.
XX
AC AAW97414;
XX
DT 20-MAY-1999 (first entry)
XX
DE KIAA0223 polymorphism in HA-1 negative homozygous individuals.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
OS Homo sapiens.
XX
PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
DR N-PSDB; AAX16080.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Disclosure; Page 38; 57pp; English.
XX
CC The present sequence represents the KIAA0223 polymorphism in HA-1
CC negative homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or Graft-versus-Host
CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ Sequence 13 AA;

Query Match 97.3%; Score 36; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 3 VLRDDLLEA 11

RESULT 13
ABP71119
ID ABP71119 standard; peptide; 10 AA.
XX
AC ABP71119;
XX
DT 14-APR-2003 (first entry)
XX
DE E10 protein CARD region fragment.
XX
KW BTF3; cell death; apoptosis; basic transcription factor; cytostatic;
KW nootropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
KW antirheumatic; antiarthritic; gene therapy; CARD; E10.
XX
OS Unidentified.
XX
PN WO200295001-A2.
XX
PD 28-NOV-2002.
XX
PF 21-MAY-2002; 2002WO-US016230.
XX
PR 21-MAY-2001; 2001US-0292559P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Rothman JH, Bloss T, Witze E;
XX
DR WPI; 2003-167228/16.
XX
PT Inhibiting or increasing programmed cell death of a cell, for treating
PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
PT expression or activity of basic transcription factor (BTF)3 or its
PT homolog in the cell.
XX
PS Example; Fig 2A; 84pp; English.
XX
CC The invention relates to inhibiting or increasing programmed cell death
CC of a cell. The method involves upregulating or inhibiting, respectively,
CC the expression or activity of basic transcription factor (BTF)3 or its
CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
CC for inhibiting or increasing programmed cell death. They are used for
CC screening for an agent that increases or inhibits programmed cell death
CC or pre-screening for an agent that modulates programmed cell death. The
CC screened agent that increases or inhibits programmed cell death, is used
CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
CC Sequences ABP71106-123 represent CARD regions of various CARD proteins
XX
SQ Sequence 10 AA;

Query Match 75.7%; Score 28; DB 6; Length 10;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LXDDLLE 8
| |||||
Db 3 LVDDLLE 9

```
RESULT 14
ADT73023
ID   ADT73023 standard; peptide; 9 AA.
XX
AC   ADT73023;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human RSV L high affinity binding peptide SeqID 919.
XX
KW   human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW   MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS   Human respiratory syncytial virus.
XX
PN   WO2004092207-A2.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-EP004061.
XX
PR   16-APR-2003; 2003EP-00447095.
XX
PA   (ALGO-) ALGONOMICS NV.
XX
PI   Lasters I,  Desmet J,  Stegmann T;
XX
DR   WPI; 2004-758334/74.
XX
PT   New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT   or P) for inducing an immune response to RSV or for diagnosing,
PT   preventing or treating viral infections, particularly RSV infection.
XX
PS   Claim 16; SEQ ID NO 919; 143pp; English.
XX
CC   This invention relates to novel isolated or purified peptides of the
CC   human respiratory syncytial virus (RSV), in particular ten RSV genes
CC   encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC   known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC   eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC   SH (also known as the 1A protein). Specifically, it refers to a
CC   composition comprising an above peptide mixed with a pharmaceutical
CC   excipient or an RSV immunogenic composition comprising a recombinant
CC   expression vector with a nucleic acid insert encoding an above peptide.
CC   The present invention describes an in vitro method of detecting cytotoxic
CC   T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC   (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC   RSV peptide is useful for preparing a diagnostic composition or an RSV
CC   (prophylactic or therapeutic) vaccine composition for a DNA-based
CC   immunisation, or for preparing an immune response provoking vaccine in
CC   the event of RSV infection (the vaccine being prepared by contacting the
CC   polypeptide in an immune response-provoking amount of specific CTL).
CC   Accordingly, these peptide compositions have virucidal activity. This
CC   peptide sequence is a human RSV high binding affinity peptide of the
CC   invention.
XX
SQ   Sequence 9 AA;

  Query Match             70.3%;  Score 26;  DB 8;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 2e+06;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              :: ||:| |
Db          1 IIKDDILSA 9


RESULT 15
AAW73901
ID   AAW73901 standard; peptide; 10 AA.
XX
AC   AAW73901;
XX
DT   17-OCT-2003  (revised)
DT   12-APR-1999  (first entry)
XX
DE   B. forsythus protease fragment.
XX
KW   Protease; haemolytic activity; diagnosis; periodontosis.
XX
OS   Tannerella forsythensis.
XX
PN   JP11009284-A.
XX
PD   19-JAN-1999.
XX
PF   25-JUN-1997;   97JP-00185849.
XX
PR   25-JUN-1997;   97JP-00185849.
XX
PA   (SUNZ ) SUNSTAR CHEM IND CO LTD.
XX
DR   WPI; 1999-145900/13.
XX
PT   New protease gene derived from Bacteroides forsythus - useful for
PT   diagnosis and treatment of periodontosis.
XX
PS   Disclosure; Page 13; 13pp; Japanese.
XX
CC   This sequence is a fragment of the Bacteroides forsythus protease of the
CC   invention. The protein has protease activity and haemolytic activity. The
CC   DNA and the polypeptide are useful for diagnosis, treatment and research
CC   of periodontosis. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ   Sequence 10 AA;

  Query Match             70.3%;  Score 26;  DB 2;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              :: ||:| |
Db          2 IIDDDLMSA 10


Search completed: April  6, 2006, 16:57:02
Job time : 116 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:57:26 ; Search time 19 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	54.1	15	2	A53594	calnexin - mouse (
2	18	48.6	10	2	C26997	unspecific monooxy
3	18	48.6	12	2	S39762	cytochrome P450 UT
4	18	48.6	15	2	A26997	unspecific monooxy
5	17	45.9	10	2	S13224	virG protein - Agr
6	17	45.9	11	2	PH0924	T-cell receptor be
7	17	45.9	13	2	PS0443	potassium channel
8	17	45.9	14	2	S50900	chlorophyll a/b-bi
9	17	45.9	14	2	C39170	acyl-[acyl-carrier
10	17	45.9	15	2	E56819	PS I complex subun
11	17	45.9	15	2	S62675	collagen type I -
12	16	43.2	7	2	S68004	hucolin, 75K chain
13	16	43.2	8	2	PC4131	hypothetical prote
14	16	43.2	10	2	A61354	carnitine medium/l
15	16	43.2	13	2	S14316	photosystem I 9K c
16	16	43.2	14	2	S29789	hypothetical prote
17	16	43.2	15	2	B32800	hypothetical prote
18	15	40.5	13	2	S12388	argA protein - Sal
19	15	40.5	13	2	S65612	tubulin alpha-chai
20	15	40.5	13	2	S00316	photosystem I 13K
21	15	40.5	14	2	A61306	ribonuclease M (EC
22	15	40.5	15	2	PQ0750	self-incompatibili
23	15	40.5	15	2	S29485	GTP-binding protei
24	15	40.5	15	2	PH1788	T cell receptor al
25	15	40.5	15	2	D54226	light-harvesting p
26	14	37.8	7	2	S20446	elastase - Pseudom
27	14	37.8	7	2	A59489	protein kinase C i
28	14	37.8	10	2	F44644	neurotoxin-associa
29	14	37.8	10	2	E86128	hypothetical prote
30	14	37.8	11	2	PT0249	Ig heavy chain CRD
31	14	37.8	11	2	PH0922	T-cell receptor be
32	14	37.8	11	4	S41909	hypothetical prote
33	14	37.8	13	2	S41209	F420-non-reducing-
34	14	37.8	13	2	G44644	neurotoxin-associa
35	14	37.8	13	2	S01043	glutamate-ammonia
36	14	37.8	14	2	T46634	acyl carrier prote
37	14	37.8	14	2	PS0252	16K protein 5404 -
38	14	37.8	14	2	PH1626	Ig H chain V-D-J r
39	14	37.8	14	2	B61597	cytochrome P450 AL
40	14	37.8	14	2	I51430	hemoglobin beta ch
41	14	37.8	15	2	PS0251	15K protein 5106 -
42	14	37.8	15	2	B26501	lipoprotein lipase
43	14	37.8	15	2	A26228	spot 42 protein -
44	14	37.8	15	2	PN0164	hyoscyamine (6S)-d
45	14	37.8	15	2	A61522	7.5k surfactant-as

ALIGNMENTS

RESULT 1
A53594
calnexin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A53594
R;Lenter, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A;Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin pr
A;Reference number: A53594; MUID:94216347; PMID:8163531
A;Accession: A53594
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <LEN>
A;Cross-references: UNIPROT:Q7M063; UNIPARC:UPI000017C62E
C;Keywords: endoplasmic reticulum; molecular chaperone

Query Match 54.1%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLXDDL 6
              :: |||
Db         10 IIEDDL 15
```

RESULT 2
C26997
unspecific monooxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic - ra
N;Alternate names: cytochrome P450
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: C26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A;Reference number: A26997; MUID:88000604; PMID:3651420
A;Accession: C26997
A;Molecule type: protein
A;Residues: 1-10 <GRA>
A;Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA8
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Query Match 48.6%; Score 18; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          5 DLLEA 9
              |||.|
Db          2 DLLSA 6
```

```
RESULT 3
S39762
cytochrome P450 UT-7b - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S39762
R;Ohishi, N.; Imaoka, S.; Suzuki, T.; Funae, Y.
Biochim. Biophys. Acta 1158, 227-236, 1993
A;Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
A;Reference number: S39761; MUID:94072607; PMID:8251521
A;Accession: S39762
A;Molecule type: protein
A;Residues: 1-12 <OHI>
A;Cross-references: UNIPARC:UPI000017C8F7

  Query Match             48.6%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.1e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDL 6
              :: |||
Db          3 LIGDDL 8


RESULT 4
A26997
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
N;Alternate names: cytochrome P450b
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: A26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A;Reference number: A26997; MUID:88000604; PMID:3651420
A;Accession: A26997
A;Molecule type: protein
A;Residues: 1-15 <GRA>
A;Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA7
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

  Query Match             48.6%;  Score 18;  DB 2;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              ||| |
Db          2 DLLSA 6


RESULT 5
S13224
virG protein - Agrobacterium sp. (fragment)
C;Species: Agrobacterium sp.
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S13224
R;Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.
J. Mol. Biol. 215, 537-547, 1990
A;Title: Binding of the regulatory protein VirG to the phased signal sequences upstream
A;Reference number: S13224; MUID:91039316; PMID:2231718
A;Accession: S13224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAM>
A;Cross-references: UNIPROT:Q7M0P7; UNIPARC:UPI000017A9C4

  Query Match             45.9%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDD 5
              |: ||
Db          6 VIDDD 10


RESULT 6
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Cross-references: UNIPARC:UPI000017C9F3
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

  Query Match             45.9%;  Score 17;  DB 2;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 1.6e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              ||:|
Db          7 DLME 10


RESULT 7
PS0443
potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C;Accession: PS0443
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A;Reference number: JH0697; MUID:92360298; PMID:1497890
A;Accession: PS0443
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-13 <ADE>
A;Cross-references: UNIPARC:UPI000017BEBA
C;Comment: This potassium channel is activated by calcium.
C;Genetics:
A;Gene: FlyBase:slo
A;Cross-references: FlyBase:FBgn0003429
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

  Query Match             45.9%;  Score 17;  DB 2;  Length 13;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              |||:
Db         10 DDLV 13


RESULT 8
S50900
chlorophyll a/b-binding protein Lhcb5 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIc protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50900
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclo
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50900
A;Molecule type: protein
```

A;Residues: 1-14 <WAL>
A;Cross-references: UNIPARC:UPI0000178182
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosys

Query Match 45.9%; Score 17; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LXDDLLE 8
| | ||:
Db 3 LPDGLLD 9

RESULT 9
C39170
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - avocado (fragments)
C;Species: Persea americana (avocado)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002
C;Accession: C39170
R;Shanklin, J.; Somerville, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A;Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally unr
A;Reference number: A39170; MUID:91172837; PMID:2006187
A;Accession: C39170
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <SHA>
A;Cross-references: UNIPARC:UPI000017CD5B
C;Keywords: oxidoreductase

Query Match 45.9%; Score 17; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLLE 8
|:||
Db 11 DILE 14

RESULT 10
E56819
PS I complex subunit 8 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: E56819
R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A;Reference number: A56819; MUID:91355209; PMID:1883835
A;Accession: E56819
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <IWA>
A;Cross-references: UNIPROT:P42052; UNIPARC:UPI0000132593
A;Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 45.9%; Score 17; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDD 5
|: ||
Db 10 VIQDD 14

RESULT 11
S62675
collagen type I - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62675
R;Mizuno, M.; Kitafima, T.; Tomita, M.; Kuboki, Y.
Biochim. Biophys. Acta 1310, 97-102, 1996
A;Title: The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of type I col
A;Reference number: S62675; MUID:97386332; PMID:9244181
A;Accession: S62675
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <MIZ>
A;Cross-references: UNIPROT:Q7M062; UNIPARC:UPI000017C63D

Query Match 45.9%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLLE 8
|:||
Db 12 DILE 15

RESULT 12
S68004
hucolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>
A;Cross-references: UNIPARC:UPI000017C164

Query Match 43.2%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
|||
Db 4 DDL 6

RESULT 13
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: PC4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding
y for biosynthesis of heme d1.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
A;Accession: PC4131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <KAW>
A;Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:g1217594
A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
C;Superfamily: Pseudomonas stutzeri nirD protein

Query Match 43.2%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
|||
Db 2 DDL 4

RESULT 14
A61354

carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
N;Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRP58;
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A61354
R;Murthy, M.S.R.; Pande, S.V.
Mol. Cell. Biochem. 122, 133-138, 1993
A;Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previ
A;Reference number: A61354; MUID:94049728; PMID:8232244
A;Accession: A61354
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <MUR>
A;Cross-references: UNIPARC:UPI000017C8DE
C;Keywords: acyltransferase

Query Match 43.2%; Score 16; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLLE 8
|:||
Db 2 DVLE 5

RESULT 15
S14316
photosystem I 9K chain - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: S14316
R;Ikeuchi, M.; Inoue, Y.
FEBS Lett. 280, 332-334, 1991
A;Title: Two new components of 9 and 14 kDa from spinach photosystem I complex.
A;Reference number: S14316; MUID:91192162; PMID:2013332
A;Accession: S14316
A;Molecule type: protein
A;Residues: 1-13 <IKE>
A;Cross-references: UNIPROT:Q7M1J1; UNIPARC:UPI000017AF28
C;Keywords: membrane-associated complex; photosynthesis; photosystem I

Query Match 43.2%; Score 16; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DDLLE 8
|: ||
Db 4 DEYLE 8

Search completed: April 6, 2006, 17:03:58
Job time : 20 secs

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:51:26 ; Search time 116.333 Seconds
(without alignments)
54.582 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	56.8	11	1	UF05_MOUSE	P38643 mus musculu
2	21	56.8	13	2	P82560_STRPY	P82560 streptococc
3	20	54.1	15	2	Q7M063_MOUSE	Q7m063 mus musculu
4	19	51.4	11	2	Q47600_ECOLI	Q47600 escherichia
5	19	51.4	15	2	Q9UC60_HUMAN	Q9uc60 homo sapien
6	19	51.4	15	2	Q9R5D6_CHRVI	Q9r5d6 chromatium
7	18	48.6	10	2	Q718N9_9PARA	Q718n9 newcastle d
8	18	48.6	11	2	Q9QVC5_RAT	Q9qvc5 rattus norv
9	18	48.6	11	2	Q718K6_9PARA	Q718k6 newcastle d
10	18	48.6	12	1	XYLA_STRVN	P14405 streptomyce
11	18	48.6	12	2	Q9T2U3_BOVIN	Q9t2u3 bos taurus
12	18	48.6	12	2	Q9TQY4_BOVIN	Q9tqy4 bos taurus
13	18	48.6	12	2	Q5MK49_9CLOS	Q5mk49 citrus tris
14	18	48.6	12	2	Q5MK52_9CLOS	Q5mk52 citrus tris
15	18	48.6	12	2	Q5MK66_9CLOS	Q5mk66 citrus tris
16	18	48.6	12	2	Q5MK81_9CLOS	Q5mk81 citrus tris
17	18	48.6	13	1	TE1JA_RANJA	P83307 rana japoni
18	18	48.6	13	2	Q8WYB7_HUMAN	Q8wyb7 homo sapien
19	18	48.6	13	2	Q7TE19_9CLOS	Q7te19 citrus tris
20	18	48.6	13	2	Q7TE20_9CLOS	Q7te20 citrus tris
21	18	48.6	13	2	Q7TE23_9CLOS	Q7te23 citrus tris
22	18	48.6	13	2	Q7TE26_9CLOS	Q7te26 citrus tris
23	18	48.6	13	2	Q7TE30_9CLOS	Q7te30 citrus tris
24	18	48.6	14	2	Q68CX5_HUMAN	Q68cx5 homo sapien
25	18	48.6	14	2	Q52840_RHILO	Q52840 rhizobium l
26	18	48.6	14	2	Q9ZB42_STRPY	Q9zb42 streptococc
27	17	45.9	10	2	Q9UWM5_SULSO	Q9uwm5 sulfolobus
28	17	45.9	10	2	Q5S732_9FUNG	Q5s732 glomus cale
29	17	45.9	10	2	Q5S733_9FUNG	Q5s733 glomus geos
30	17	45.9	10	2	Q9TQV4_HORSE	Q9tqv4 e equus cab
31	17	45.9	10	2	Q7M0P7_AGRSP	Q7m0p7 agrobacteri
32	17	45.9	11	2	Q5IKF0_HUMAN	Q5ikf0 homo sapien
33	17	45.9	12	2	Q9XS31_PIG	Q9xs31 sus scrofa
34	17	45.9	13	2	Q6DW14_BOVIN	Q6dw14 bos taurus
35	17	45.9	13	2	Q957T7_9PERC	Q957t7 trichopsis
36	17	45.9	14	2	Q8HR43_CLIMI	Q8hr43 clivia mini
37	17	45.9	15	1	PSAO_CUCSA	P42052 cucumis sat
38	17	45.9	15	2	Q9FSB2_9CARY	Q9fsb2 silene aega
39	17	45.9	15	2	Q9R565_STRCO	Q9r565 streptomyce
40	17	45.9	15	2	Q7M062_MOUSE	Q7m062 mus musculu
41	17	45.9	15	2	Q80362_9HIV1	Q80362 human immun
42	16	43.2	9	2	Q70SM2_HUMAN	Q70sm2 homo sapien
43	16	43.2	9	2	Q8LPT5_MAIZE	Q8lpt5 zea mays (m
44	16	43.2	9	2	P82568_STRPY	P82568 streptococc
45	16	43.2	10	1	GYMN_GYMCH	P84200 gymnocladus

ALIGNMENTS

RESULT 1
UF05_MOUSE
ID UF05_MOUSE STANDARD; PRT; 11 AA.
AC P38643;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P48) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.5, its MW is: 48 kDa.
CC ----------
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ----------
KW Direct protein sequencing.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1330 MW; E54835E5CAAABAFA CRC64;

Query Match 56.8%; Score 21; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLXDDLLE 8
              : |||::|
Db          3 IXXDDVIE 10
```

RESULT 2
P82560_STRPY
ID P82560_STRPY PRELIMINARY; PRT; 13 AA.
AC P82560;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

```
OX   NCBI_TaxID=1314;
RN   [1]
RP   PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC   STRAIN=JRS4;
RA   Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA   VanBogelen R.A.;
RT   "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT   proteins.";
RL   Submitted (MAY-2000) to Swiss-Prot.
CC   -!- MASS SPECTROMETRY: MW=30142.85; METHOD=Electrospray.
FT   NON_TER       1      1
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1464 MW;  CFE7DB129CE0C6D9 CRC64;

  Query Match             56.8%;  Score 21;  DB 2;  Length 13;
  Best Local Similarity   37.5%;  Pred. No. 2.8e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              : ||: :|
Db          1 ITDDVFQA 8


RESULT 3
Q7M063_MOUSE
ID   Q7M063_MOUSE PRELIMINARY;      PRT;    15 AA.
AC   Q7M063;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Calnexin (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=94216347; PubMed=8163531;
RA   Lenter M., Vestweber D.;
RT   "The integrin chains beta-1 and alpha-6 associate with the chaperone
RT   calnexin prior to integrin assembly.";
RL   J. Biol. Chem. 269:12263-12268(1994).
DR   PIR; A53594; A53594.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1693 MW;  C62AAAA42F9F5F35 CRC64;

  Query Match             54.1%;  Score 20;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 5.2e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDL 6
              :: |||
Db         10 IIEDDL 15


RESULT 4
Q47600_ECOLI
ID   Q47600_ECOLI PRELIMINARY;      PRT;    11 AA.
AC   Q47600;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   REase protein (Fragment).
GN   Name=REase;
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91139577; PubMed=1995588;
RA   Tao T., Bourne J.C., Blumenthal R.M.;
RT   "A family of regulatory genes associated with type II restriction-
RT   modification systems.";
RL   J. Bacteriol. 173:1367-1375(1991).
DR   EMBL; M63619; AAA24556.1; -; Genomic_DNA.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1232 MW;  63175479572AB5A4 CRC64;

  Query Match             51.4%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 6e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              |  ||: |
Db          3 LRSDLINA 10


RESULT 5
Q9UC60_HUMAN
ID   Q9UC60_HUMAN  PRELIMINARY;      PRT;    15 AA.
AC   Q9UC60;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=95392215; PubMed=7663175; DOI=10.1006/prep.1995.1049;
RA   De Pauw P., Neyt C., Vanderwinkel E., Wattiez R., Falmagne P.;
RT   "Characterization of human serum N-acetylmuramyl-L-alanine amidase
RT   purified by affinity chromatography.";
RL   Protein Expr. Purif. 6:371-378(1995).
DR   GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; TAS.
DR   GO; GO:0001519; P:peptide amidation; NAS.
SQ   SEQUENCE   15 AA;  1600 MW;  9016B00FFF9E780A CRC64;

  Query Match             51.4%;  Score 19;  DB 2;  Length 15;
  Best Local Similarity   33.3%;  Pred. No. 8.3e+03;
  Matches    3;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              :| | :::|
Db          4 LLMDSVIQA 12


RESULT 6
Q9R5D6_CHRVI
ID   Q9R5D6_CHRVI  PRELIMINARY;      PRT;    15 AA.
AC   Q9R5D6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein
DE   (Fragment).
OS   Chromatium vinosum.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC   Chromatiaceae; Allochromatium.
OX   NCBI_TaxID=1049;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93146381; PubMed=1490603; DOI=10.1016/0378-1097(92)90031-I;
RA   Liebergesell M., Schmidt B., Steinbuchel A.;
RT   "Isolation and identification of granule-associated proteins relevant
RT   for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
RT   D.";
RL   FEMS Microbiol. Lett. 78:227-232(1992).
SQ   SEQUENCE   15 AA;  1874 MW;  165FA9A16BCA2A9D CRC64;
```

```
  Query Match             51.4%;  Score 19;  DB 2;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 8.3e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              || ||
Db          9 DDWLE 13


RESULT 7
Q718N9_9PARA
ID   Q718N9_9PARA PRELIMINARY;      PRT;    10 AA.
AC   Q718N9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hemagglutinin-neuraminidase (Fragment).
OS   Newcastle disease virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX   NCBI_TaxID=11176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gould A.R., Hansson E., Selleck K., Kattenbelt J.A., Mackenzie M.,
RA   Della-Porta A.J.;
RT   "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
RT   motifs as markers for viral lineage.";
RL   Avian Pathol. 32:361-373(2003).
DR   EMBL; AF542884; AAQ11609.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1100 MW;  711806AAA337205B CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 8.7e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDD 5
              :| ||
Db          4 ILKDD 8


RESULT 8
Q9QVC5_RAT
ID   Q9QVC5_RAT  PRELIMINARY;      PRT;    11 AA.
AC   Q9QVC5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   DW53 protein (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=92291078; PubMed=1601872;
RA   Subramaniam V.N., bin Mohd Yusoff A.R., Wong S.H., Lim G.B., Chew M.,
RA   Hong W.;
RT   "Biochemical fractionation and characterization of proteins from
RT   Golgi-enriched membranes.";
RL   J. Biol. Chem. 267:12016-12021(1992).
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1210 MW;  5B61C10B9DDAB2C7 CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 11;
  Best Local Similarity   44.4%;  Pred. No. 9.7e+03;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || | :| :
Db          3 VLVDAMLHS 11


RESULT 9
Q718K6_9PARA
ID   Q718K6_9PARA PRELIMINARY;      PRT;    11 AA.
AC   Q718K6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hemagglutinin-neuraminidase (Fragment).
OS   Newcastle disease virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX   NCBI_TaxID=11176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gould A.R., Hansson E., Selleck K., Kattenbelt J.A., Mackenzie M.,
RA   Della-Porta A.J.;
RT   "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
RT   motifs as markers for viral lineage.";
RL   Avian Pathol. 32:361-373(2003).
DR   EMBL; AF542917; AAQ11642.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   11 AA;  1313 MW;  710428D6A337205B CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 9.7e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDD 5
              :| ||
Db          5 ILKDD 9


RESULT 10
XYLA_STRVN
ID   XYLA_STRVN     STANDARD;      PRT;    12 AA.
AC   P14405;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Xylose isomerase (EC 5.3.1.5) (Fragment).
GN   Name=xylA;
OS   Streptomyces violaceoruber.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1935;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   STRAIN=LMG 7183;
RX   MEDLINE=90104230; PubMed=2604694;
RA   Vangrysperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
RT   "Single active-site histidine in D-xylose isomerase from Streptomyces
RT   violaceoruber. Identification by chemical derivatization and peptide
RT   mapping.";
RL   Biochem. J. 263:195-199(1989).
CC   -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC   -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the xylose isomerase family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   HAMAP; MF_00455; -; 1.
DR   InterPro; IPR001998; Xylose_isom.
DR   PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR   PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW   Carbohydrate metabolism; Direct protein sequencing; Isomerase;
KW   Magnesium; Metal-binding; Pentose shunt; Xylose metabolism.
```

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FT   ACT_SITE      5      5
FT   ACT_SITE      8      8       By similarity.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1376 MW;  E749268EB1AAAAA1 CRC64;

  Query Match             48.6%;  Score 18;  DB 1;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              |||:
Db          7 DDLI 10


RESULT 11
Q9T2U3_BOVIN
ID   Q9T2U3_BOVIN PRELIMINARY;      PRT;    12 AA.
AC   Q9T2U3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   NADH:ubiquinone oxidoreductase (Complex I) iron-sulfur protein
DE   fraction 20 kDa polypeptide peptide T-8 (Fragment).
OS   Bos taurus (Bovine).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=92138662; PubMed=1778979;
RA   Masui R., Wakabayashi S., Matsubara H., Hatefi Y.;
RT   "The amino acid sequence of the 9 kDa polypeptide and partial amino
RT   acid sequence of the 20 kDa polypeptide of mitochondrial
RT   NADH:ubiquinone oxidoreductase.";
RL   J. Biochem. 110:575-582(1991).
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1335 MW;  CC9702EC3C233DC2 CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              |||:
Db          9 DDLI 12


RESULT 12
Q9TQY4_BOVIN
ID   Q9TQY4_BOVIN PRELIMINARY;      PRT;    12 AA.
AC   Q9TQY4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Glycoprotein H-B N-TERMINAL, GPH-B N-TERMINAL=KEX2/subtilisin-related
DE   protease (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=91340701; PubMed=1874725;
RA   Christie D.L., Batchelor D.C., Palmer D.J.;
RT   "Identification of kex2-related proteases in chromaffin granules by
RT   partial amino acid sequence analysis.";
RL   J. Biol. Chem. 266:15679-15683(1991).
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1303 MW;  9F2FF9E2782DC5BA CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+04;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              ||||  |:
Db          2 VLXDSALD 9


RESULT 13
Q5MK49_9CLOS
ID   Q5MK49_9CLOS PRELIMINARY;      PRT;    12 AA.
AC   Q5MK49;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   RdRp (Fragment).
OS   Citrus tristeza virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC   Closterovirus.
OX   NCBI_TaxID=12162;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B359;
RA   Hilf M.E., Mavrodieva V.A., Garnsey S.M.;
RT   "POL and K17 markers from Beltsville CTV isolates.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY756309; AAW22818.1; -; Genomic_RNA.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1146 MW;  CAA485D77F187DC6 CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              ||| :|
Db          1 DDLGQA 6


RESULT 14
Q5MK52_9CLOS
ID   Q5MK52_9CLOS PRELIMINARY;      PRT;    12 AA.
AC   Q5MK52;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   RdRp (Fragment).
OS   Citrus tristeza virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC   Closterovirus.
OX   NCBI_TaxID=12162;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B358;
RA   Hilf M.E., Mavrodieva V.A., Garnsey S.M.;
RT   "POL and K17 markers from Beltsville CTV isolates.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY756307; AAW22815.1; -; Genomic_RNA.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1146 MW;  CAA485D77F187DC6 CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              ||| :|
Db          1 DDLGQA 6
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RESULT 15
Q5MK66_9CLOS
ID   Q5MK66_9CLOS PRELIMINARY;      PRT;    12 AA.
AC   Q5MK66;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   RdRp (Fragment).
OS   Citrus tristeza virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
OC   Closterovirus.
OX   NCBI_TaxID=12162;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B183;
RA   Hilf M.E., Mavrodieva V.A., Garnsey S.M.;
RT   "POL and K17 markers from Beltsville CTV isolates.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY756294; AAW22796.1; -; Genomic_RNA.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1146 MW;  CAA485D77F187DC6 CRC64;

  Query Match             48.6%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              ||| :|
Db          1 DDLGQA 6


Search completed: April  6, 2006, 17:02:57
Job time : 119.333 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:03:16 ; Search time 27.6667 Seconds
(without alignments)
26.894 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	2	US-09-269-250E-18	Sequence 18, Appl
2	36	97.3	9	2	US-09-269-250E-20	Sequence 20, Appl
3	36	97.3	9	2	US-09-269-250E-29	Sequence 29, Appl
4	36	97.3	9	2	US-09-489-760-1	Sequence 1, Appli
5	36	97.3	9	2	US-09-489-760-2	Sequence 2, Appli
6	36	97.3	9	2	US-09-489-760-5	Sequence 5, Appli
7	36	97.3	13	2	US-09-269-250E-26	Sequence 26, Appl
8	36	97.3	13	2	US-09-269-250E-28	Sequence 28, Appl
9	36	97.3	13	2	US-09-489-760-14	Sequence 14, Appl
10	36	97.3	13	2	US-09-489-760-16	Sequence 16, Appl
11	23	62.2	8	2	US-09-269-250E-38	Sequence 38, Appl
12	23	62.2	15	2	US-08-940-095-104	Sequence 104, App
13	23	62.2	15	2	US-08-940-093-104	Sequence 104, App
14	23	62.2	15	2	US-08-940-096-104	Sequence 104, App
15	23	62.2	15	2	US-09-465-719-104	Sequence 104, App
16	23	62.2	15	2	US-09-453-605-104	Sequence 104, App
17	23	62.2	15	2	US-09-453-838-104	Sequence 104, App
18	23	62.2	15	2	US-08-940-136-104	Sequence 104, App
19	23	62.2	15	2	US-09-453-841-104	Sequence 104, App
20	23	62.2	15	2	US-09-453-833-104	Sequence 104, App
21	23	62.2	15	2	US-09-453-826-104	Sequence 104, App
22	23	62.2	15	2	US-09-453-840-104	Sequence 104, App
23	23	62.2	15	2	US-09-865-989-104	Sequence 104, App
24	23	62.2	15	2	US-09-453-834-104	Sequence 104, App
25	23	62.2	15	2	US-10-283-599-104	Sequence 104, App
26	23	62.2	15	2	US-09-465-718-104	Sequence 104, App
27	22	59.5	7	2	US-08-556-419-14	Sequence 14, Appl
28	22	59.5	9	2	US-09-744-549-15	Sequence 15, Appl
29	22	59.5	9	2	US-10-394-980-421	Sequence 421, App
30	22	59.5	9	2	US-10-394-980-464	Sequence 464, App
31	22	59.5	11	1	US-08-726-136-13	Sequence 13, Appl
32	22	59.5	11	2	US-09-103-434-13	Sequence 13, Appl
33	22	59.5	11	2	US-09-687-594-13	Sequence 13, Appl
34	22	59.5	12	2	US-09-569-037-1	Sequence 1, Appli
35	22	59.5	14	1	US-08-366-276-9	Sequence 9, Appli
36	22	59.5	15	2	US-09-069-827A-132	Sequence 132, App
37	22	59.5	15	2	US-09-050-739-79	Sequence 79, Appl
38	21	56.8	6	1	US-08-459-568-20	Sequence 20, Appl
39	21	56.8	6	1	US-08-399-411-20	Sequence 20, Appl
40	21	56.8	6	2	US-08-516-859A-20	Sequence 20, Appl
41	21	56.8	6	2	US-09-586-472-20	Sequence 20, Appl
42	21	56.8	6	2	US-09-528-706-20	Sequence 20, Appl
43	21	56.8	8	1	US-08-459-568-75	Sequence 75, Appl
44	21	56.8	8	1	US-08-399-411-75	Sequence 75, Appl
45	21	56.8	8	2	US-08-516-859A-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 97.3%; Score 36; DB 2; Length 9;

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  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 3
US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 4
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
;   OTHER INFORMATION: RESIDUE
US-09-489-760-1

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 5
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
US-09-489-760-2

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 6
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
US-09-269-250E-26
; Sequence 26, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
```

```
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-26

  Query Match             97.3%;  Score 36;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 0.23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          3 VLRDDLLEA 11


RESULT 8
US-09-269-250E-28
; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

  Query Match             97.3%;  Score 36;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 0.23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          3 VLHDDLLEA 11


RESULT 9
US-09-489-760-14
; Sequence 14, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:HA-1-/-
US-09-489-760-14

  Query Match             97.3%;  Score 36;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 0.23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          3 VLRDDLLEA 11


RESULT 10
US-09-489-760-16
; Sequence 16, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:HA-1+/+
US-09-489-760-16

  Query Match             97.3%;  Score 36;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 0.23;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          3 VLHDDLLEA 11


RESULT 11
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-269-250E-38

  Query Match             62.2%;  Score 23;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              |||||
Db          4 DLLEA 8
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RESULT 12
US-08-940-095-104
; Sequence 104, Application US/08940095
; Patent No. 6004925
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    APPLICANT:  Dufourcq, Jean
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,095
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0004-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6004925e
US-08-940-095-104

  Query Match             62.2%;  Score 23;  DB 2;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              | ::||||
Db          2 LLNELLEA 9


RESULT 13
US-08-940-093-104
; Sequence 104, Application US/08940093
; Patent No. 6037323
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,093
;      FILING DATE:  29-SEP-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6037323e
US-08-940-093-104

  Query Match             62.2%;  Score 23;  DB 2;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              | ::||||
Db          2 LLNELLEA 9


RESULT 14
US-08-940-096-104
; Sequence 104, Application US/08940096
; Patent No. 6046166
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/940,096
;      FILING DATE:  29-SEP-1997
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;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6046166e
US-08-940-096-104

  Query Match             62.2%;  Score 23;  DB 2;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              | ::||||
Db          2 LLNELLEA 9


RESULT 15
US-09-465-719-104
; Sequence 104, Application US/09465719
; Patent No. 6265377
;  GENERAL INFORMATION:
;    APPLICANT:  Dasseux, Jean-Louis
;    APPLICANT:  Sekul, Renate
;    APPLICANT:  Buttner, Klaus
;    APPLICANT:  Cornut, Isabelle
;    APPLICANT:  Metz, Gunther
;    TITLE OF INVENTION:  APOLIPOPROTEIN A-I AGONISTS
;    TITLE OF INVENTION:  AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;    NUMBER OF SEQUENCES:  258
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/465,719
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/940,093
;      FILING DATE:  29-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  009196-0006-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  104:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 6265377e
US-09-465-719-104

  Query Match             62.2%;  Score 23;  DB 2;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              | ::||||
Db          2 LLNELLEA 9


Search completed:  April  6, 2006, 17:05:27
Job time :  27.6667 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:22:22 ; Search time 96.6667 Seconds
(without alignments)
38.901 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	4	US-10-623-176-1	Sequence 1, Appli
2	36	97.3	9	4	US-10-623-176-2	Sequence 2, Appli
3	36	97.3	9	4	US-10-623-176-10	Sequence 10, Appl
4	36	97.3	9	4	US-10-791-217-1	Sequence 1, Appli
5	36	97.3	9	4	US-10-791-217-2	Sequence 2, Appli
6	36	97.3	9	4	US-10-791-217-5	Sequence 5, Appli
7	36	97.3	9	5	US-10-861-335-1	Sequence 1, Appli
8	36	97.3	9	6	US-11-007-740-18	Sequence 18, Appl
9	36	97.3	9	6	US-11-007-740-20	Sequence 20, Appl
10	36	97.3	9	6	US-11-007-740-29	Sequence 29, Appl
11	36	97.3	10	4	US-10-623-176-24	Sequence 24, Appl
12	36	97.3	10	4	US-10-623-176-43	Sequence 43, Appl
13	36	97.3	10	4	US-10-623-176-44	Sequence 44, Appl
14	36	97.3	12	4	US-10-623-176-65	Sequence 65, Appl
15	36	97.3	13	4	US-10-623-176-74	Sequence 74, Appl
16	36	97.3	13	4	US-10-623-176-76	Sequence 76, Appl
17	36	97.3	13	4	US-10-791-217-14	Sequence 14, Appl
18	36	97.3	13	4	US-10-791-217-16	Sequence 16, Appl
19	36	97.3	13	6	US-11-007-740-26	Sequence 26, Appl
20	36	97.3	13	6	US-11-007-740-28	Sequence 28, Appl
21	32	86.5	9	4	US-10-623-176-41	Sequence 41, Appl
22	32	86.5	9	4	US-10-623-176-42	Sequence 42, Appl
23	32	86.5	9	4	US-10-623-176-45	Sequence 45, Appl
24	32	86.5	9	4	US-10-623-176-46	Sequence 46, Appl
25	29	78.4	9	4	US-10-623-176-47	Sequence 47, Appl
26	29	78.4	9	4	US-10-623-176-48	Sequence 48, Appl
27	28	75.7	10	4	US-10-153-344-11	Sequence 11, Appl
28	27	73.0	9	4	US-10-623-176-23	Sequence 23, Appl
29	27	73.0	9	4	US-10-623-176-40	Sequence 40, Appl
30	27	73.0	10	4	US-10-623-176-6	Sequence 6, Appli
31	27	73.0	10	4	US-10-623-176-7	Sequence 7, Appli
32	27	73.0	10	4	US-10-623-176-8	Sequence 8, Appli
33	27	73.0	13	4	US-10-623-176-54	Sequence 54, Appl
34	27	73.0	13	4	US-10-623-176-64	Sequence 64, Appl
35	25	67.6	10	3	US-09-572-404B-428	Sequence 428, App
36	25	67.6	10	4	US-10-702-400-90	Sequence 90, Appl
37	25	67.6	10	5	US-10-805-650-90	Sequence 90, Appl
38	25	67.6	13	4	US-10-468-496-761	Sequence 761, App
39	25	67.6	13	4	US-10-468-496-762	Sequence 762, App
40	25	67.6	13	4	US-10-468-496-763	Sequence 763, App
41	25	67.6	13	4	US-10-468-496-764	Sequence 764, App
42	24	64.9	10	5	US-10-773-274A-7	Sequence 7, Appli
43	24	64.9	13	4	US-10-145-415-66	Sequence 66, Appl
44	23	62.2	8	4	US-10-623-176-15	Sequence 15, Appl
45	23	62.2	8	6	US-11-007-740-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; OTHER INFORMATION: wherein X can be R or H
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-1

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
||||||||
Db 1 VLXDDLLEA 9

RESULT 2
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.

```
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-2

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 3
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-10

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 4
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 5
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 6
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
;  TITLE OF INVENTION:  of tumors
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

  Query Match             97.3%;  Score 36;  DB 5;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 8
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

  Query Match             97.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 9
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

  Query Match             97.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 10
US-11-007-740-29
; Sequence 29, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
```

```
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29

  Query Match             97.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 11
US-10-623-176-24
; Sequence 24, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   OTHER INFORMATION: wherein X can be H or R
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(10)
US-10-623-176-24

  Query Match             97.3%;  Score 36;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 12
US-10-623-176-43
; Sequence 43, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(10)
US-10-623-176-43

  Query Match             97.3%;  Score 36;  DB 4;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 13
US-10-623-176-44
; Sequence 44, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(10)
US-10-623-176-44

  Query Match             97.3%;  Score 36;  DB 4;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
```

```
                  || ||||||
Db          1 VLRDDLLEA 9


RESULT 14
US-10-623-176-65
; Sequence 65, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(12)
US-10-623-176-65

  Query Match             97.3%;  Score 36;  DB 4;  Length 12;
  Best Local Similarity   88.9%;  Pred. No. 2.2;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
                || ||||||
Db          2 VLRDDLLEA 10


RESULT 15
US-10-623-176-74
; Sequence 74, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
;   OTHER INFORMATION: sequence derived from a presumed HA-1 negative
;   OTHER INFORMATION: individual
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(13)
US-10-623-176-74

  Query Match             97.3%;  Score 36;  DB 4;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 2.4;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
                || ||||||
Db          3 VLRDDLLEA 11


Search completed: April  6, 2006, 17:28:45
Job time : 97.6667 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:24:07 ; Search time 12.6667 Seconds
(without alignments)
22.163 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 65691

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	7	US-11-010-748A-11	Sequence 11, Appl
2	36	97.3	9	7	US-11-010-748A-12	Sequence 12, Appl
3	22	59.5	15	7	US-11-172-740-1404	Sequence 1404, Ap
4	21	56.8	9	6	US-10-927-435-63	Sequence 63, Appl
5	21	56.8	9	6	US-10-927-634-63	Sequence 63, Appl
6	21	56.8	15	6	US-10-353-783-71	Sequence 71, Appl
7	20	54.1	5	7	US-11-129-143-168	Sequence 168, App
8	20	54.1	5	7	US-11-129-143-169	Sequence 169, App
9	20	54.1	5	7	US-11-129-143-170	Sequence 170, App
10	20	54.1	5	7	US-11-129-143-171	Sequence 171, App
11	20	54.1	5	7	US-11-129-143-172	Sequence 172, App
12	20	54.1	5	7	US-11-129-143-173	Sequence 173, App
13	20	54.1	7	6	US-10-982-440-126	Sequence 126, App
14	20	54.1	8	7	US-11-021-305-62	Sequence 62, Appl
15	20	54.1	8	7	US-11-021-305-65	Sequence 65, Appl
16	20	54.1	8	7	US-11-021-305-66	Sequence 66, Appl
17	20	54.1	10	6	US-10-989-767A-159	Sequence 159, App
18	20	54.1	10	6	US-10-989-767A-441	Sequence 441, App
19	20	54.1	10	6	US-10-989-767A-547	Sequence 547, App
20	20	54.1	12	7	US-11-004-399-1909	Sequence 1909, Ap
21	20	54.1	13	7	US-11-207-078-102	Sequence 102, App
22	19	51.4	6	7	US-11-207-078-373	Sequence 373, App
23	19	51.4	7	7	US-11-225-686-2954	Sequence 2954, Ap
24	19	51.4	7	7	US-11-225-686-3877	Sequence 3877, Ap
25	19	51.4	7	7	US-11-225-686-3914	Sequence 3914, Ap
26	19	51.4	7	7	US-11-225-686-3915	Sequence 3915, Ap
27	19	51.4	7	7	US-11-225-686-3916	Sequence 3916, Ap
28	19	51.4	7	7	US-11-225-686-3932	Sequence 3932, Ap
29	19	51.4	7	7	US-11-225-686-3941	Sequence 3941, Ap
30	19	51.4	7	7	US-11-202-009-2954	Sequence 2954, Ap
31	19	51.4	7	7	US-11-202-009-3877	Sequence 3877, Ap
32	19	51.4	7	7	US-11-202-009-3914	Sequence 3914, Ap
33	19	51.4	7	7	US-11-202-009-3915	Sequence 3915, Ap
34	19	51.4	7	7	US-11-202-009-3916	Sequence 3916, Ap
35	19	51.4	7	7	US-11-202-009-3932	Sequence 3932, Ap
36	19	51.4	7	7	US-11-202-009-3941	Sequence 3941, Ap
37	19	51.4	9	6	US-10-073-301A-7	Sequence 7, Appli
38	19	51.4	9	6	US-10-989-767A-39	Sequence 39, Appl
39	19	51.4	9	6	US-10-927-435-62	Sequence 62, Appl
40	19	51.4	9	6	US-10-927-634-62	Sequence 62, Appl
41	19	51.4	9	7	US-11-203-137-7	Sequence 7, Appli
42	19	51.4	12	7	US-11-004-399-1739	Sequence 1739, Ap
43	19	51.4	13	7	US-11-207-078-77	Sequence 77, Appl
44	19	51.4	13	7	US-11-207-078-93	Sequence 93, Appl
45	19	51.4	15	6	US-10-522-297-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-11

Query Match 97.3%; Score 36; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

```
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
;  FILE REFERENCE: MER-136
;  CURRENT APPLICATION NUMBER: US/11/010,748A
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/EP03/06251
;  PRIOR FILING DATE: 2003-06-13
;  PRIOR APPLICATION NUMBER: EP02013423.5
;  PRIOR FILING DATE: 2002-06-13
;  NUMBER OF SEQ ID NOS: 926
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
;   OTHER INFORMATION: ell epitopes
US-11-010-748A-12

  Query Match             97.3%;  Score 36;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 3
US-11-172-740-1404
; Sequence 1404, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
;  APPLICANT: MASCIA, Peter
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
;  TITLE OF INVENTION:  PLANT CHARACTERISTICS AND PHENOTYPES
;  FILE REFERENCE: 2750-1602PUS2
;  CURRENT APPLICATION NUMBER: US/11/172,740
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,621
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,800
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1404
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (208)..(258)
;   OTHER INFORMATION: Pfam Name: PHD; Pfam Description: PHD-finger
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (208)..(258)
;   OTHER INFORMATION: Pfam Name: PHD; Pfam Description: PHD-finger
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for increasing chlorophyll and photosynthetic cap
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making larger plants
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowers
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confinem
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making taller plants and plants with longer
;   OTHER INFORMATION: inflorescences
US-11-172-740-1404

  Query Match             59.5%;  Score 22;  DB 7;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              |  || ||
Db          8 VYVDDYLE 15


RESULT 4
US-10-927-435-63
; Sequence 63, Application US/10927435
; Publication No. US20060045884A1
; GENERAL INFORMATION:
;  APPLICANT: MOLLDREM, JEFFREY
;  TITLE OF INVENTION: VACCINES FOR AUTOIMMUNE AND INFECTIOUS DISEASE
;  FILE REFERENCE: UTSC:788USC2
;  CURRENT APPLICATION NUMBER: US/10/927,435
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/489,238
;  PRIOR FILING DATE: 2003-08-26
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-927-435-63

  Query Match             56.8%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              :| | |||
Db          1 ILLDWLLE 8


RESULT 5
US-10-927-634-63
; Sequence 63, Application US/10927634
; Publication No. US20060045881A1
; GENERAL INFORMATION:
;  APPLICANT: MOLLDREM, JEFFREY
;  TITLE OF INVENTION: ANTI-CANCER VACCINES
;  FILE REFERENCE: UTSC:788USC1
;  CURRENT APPLICATION NUMBER: US/10/927,634
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/489,238
;  PRIOR FILING DATE: 2003-08-26
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
```

```
;   OTHER INFORMATION: Peptide
US-10-927-634-63

  Query Match             56.8%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              :| | |||
Db          1 ILLDWLLE 8


RESULT 6
US-10-353-783-71
; Sequence 71, Application US/10353783
; Publication No. US20050261175A1
;   GENERAL INFORMATION:
;        APPLICANT: Zsebo, Krisztina M.
;                   Bosselman, Robert A.
;                   Suggs, Sidney V.
;                   Martin, Francis H.
;        TITLE OF INVENTION: Stem Cell Factor
;        NUMBER OF SEQUENCES: 104
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: United States of America
;             ZIP: 60606-6402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/353,783
;             FILING DATE: 28-Jan-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/448,729
;             FILING DATE: 24-MAY-1995
;             APPLICATION NUMBER: 08/172,329
;             FILING DATE: 21-DEC-1993
;             APPLICATION NUMBER: 07/982,255
;             FILING DATE: 25-NOV-1992
;             APPLICATION NUMBER: 07/684,535
;             FILING DATE: 10-APR-1991
;             APPLICATION NUMBER: 07/589,701
;             FILING DATE: 01-OCT-1990
;             APPLICATION NUMBER: 07/573,616
;             FILING DATE: 24-AUG-1990
;             APPLICATION NUMBER: 07/537,198
;             FILING DATE: 11-JUN-1990
;             APPLICATION NUMBER: 07/422,383
;             FILING DATE: 16-OCT-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Clough, David W.
;             REGISTRATION NUMBER: 36,107
;             REFERENCE/DOCKET NUMBER: 01017/32958A
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312/474-6300
;             TELEFAX: 312/474-0448
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 71:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-353-783-71

  Query Match             56.8%;  Score 21;  DB 6;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+02;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              : |||: |
Db          1 IVDDLVAA 8


RESULT 7
US-11-129-143-168
; Sequence 168, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bradyrhizobium japonicum
US-11-129-143-168

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 8
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-169

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5
```

```
RESULT 9
US-11-129-143-170
; Sequence 170, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bacillus stearothermophilus
US-11-129-143-170

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 10
US-11-129-143-171
; Sequence 171, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bacillus subtilis
US-11-129-143-171

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 11
US-11-129-143-172
; Sequence 172, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-129-143-172

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 12
US-11-129-143-173
; Sequence 173, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
US-11-129-143-173

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 13
US-10-982-440-126
; Sequence 126, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
;  APPLICANT: Oliner, John
;  APPLICANT:  Graham, Kevin
;  TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
;  FILE REFERENCE: 04-881-A
;  CURRENT APPLICATION NUMBER: US/10/982,440
;  CURRENT FILING DATE:  2004-11-04
;  PRIOR APPLICATION NUMBER: 60/620,161
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126
;   LENGTH: 7
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-126

Query Match 54.1%; Score 20; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLL 7
||||
Db 2 DDLL 5

RESULT 14
US-11-021-305-62
; Sequence 62, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
; APPLICANT: Prins, Johannes B
; APPLICANT: Hutley, Louise J
; TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
; FILE REFERENCE: DAVI169.001CP1
; CURRENT APPLICATION NUMBER: US/11/021,305
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: USSN 60/392,130
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
US-11-021-305-62

Query Match 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLL 7
||||
Db 4 DDLL 7

RESULT 15
US-11-021-305-65
; Sequence 65, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
; APPLICANT: Prins, Johannes B
; APPLICANT: Hutley, Louise J
; TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
; FILE REFERENCE: DAVI169.001CP1
; CURRENT APPLICATION NUMBER: US/11/021,305
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: USSN 60/392,130
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 8
; TYPE: PRT
; ORGANISM: mammalian
US-11-021-305-65

Query Match 54.1%; Score 20; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLL 7
||||
Db 4 DDLL 7

Search completed: April 6, 2006, 17:29:29
Job time : 13.6667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:50:52 ; Search time 114 Seconds
(without alignments)
34.688 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	2	AAW99196	Aaw99196 Minor his
2	45	100.0	9	2	AAW97375	Aaw97375 HA-1 H-al
3	45	100.0	9	8	ADH40333	Adh40333 Human min
4	45	100.0	13	2	AAW99199	Aaw99199 vR cell K
5	45	100.0	13	2	AAW97415	Aaw97415 KIAA0223
6	37	82.2	9	2	AAW99197	Aaw99197 Minor his
7	37	82.2	9	2	AAW97374	Aaw97374 HA-1 R-al
8	37	82.2	9	8	ADH40334	Adh40334 Human min
9	37	82.2	13	2	AAW99198	Aaw99198 DH cell K
10	37	82.2	13	2	AAW97414	Aaw97414 KIAA0223
11	36	80.0	9	2	AAW99195	Aaw99195 Minor his
12	36	80.0	9	2	AAW97572	Aaw97572 T-cell ep
13	31	68.9	9	8	ADU99853	Adu99853 BCZ4 tumo
14	30	66.7	9	2	AAW97373	Aaw97373 Peptide e
15	29	64.4	13	4	AAU02706	Aau02706 CDR regio
16	28	62.2	9	2	AAY10122	Aay10122 T cell ep
17	28	62.2	9	5	ABG79805	Abg79805 MHC class
18	28	62.2	9	8	ADK68732	Adk68732 Epitope 1
19	28	62.2	9	8	ADK05291	Adk05291 Hepatitis
20	28	62.2	9	8	ADK05293	Adk05293 Hepatitis
21	28	62.2	9	8	ADQ10530	Adq10530 Cercopith
22	28	62.2	9	8	ADS81010	Ads81010 Tumour-as
23	28	62.2	10	8	ADK05295	Adk05295 Hepatitis
24	28	62.2	10	8	ADP26019	Adp26019 Plasmodiu
25	28	62.2	11	7	ADD23269	Add23269 Breast ca
26	27	60.0	9	6	ABJ20115	Abj20115 MHC bindi
27	27	60.0	9	8	ADT02787	Adt02787 Human tum
28	27	60.0	10	8	ADQ26722	Adq26722 Topo V Hh
29	27	60.0	13	4	AAB85071	Aab85071 Human ser
30	27	60.0	13	4	AAB85066	Aab85066 Human ser
31	26	57.8	6	6	ABU97233	Abu97233 Enzyme pe
32	26	57.8	6	6	ABU97232	Abu97232 Enzyme pe
33	26	57.8	6	6	ABU97234	Abu97234 Enzyme pe
34	26	57.8	6	6	ABU97231	Abu97231 Enzyme pe
35	26	57.8	6	9	ADY63770	Ady63770 Human alb
36	26	57.8	7	8	ADM96262	Adm96262 Human ser
37	26	57.8	9	5	AAE31275	Aae31275 Human mag
38	26	57.8	9	8	ADM96261	Adm96261 Human ser
39	26	57.8	9	8	ADM96258	Adm96258 Human ser
40	26	57.8	9	8	ADT73023	Adt73023 Human RSV
41	26	57.8	9	8	ADT49074	Adt49074 Human BFA
42	26	57.8	9	8	ADU99636	Adu99636 BFA5 tumo
43	26	57.8	10	2	AAW73901	Aaw73901 B. forsyt
44	26	57.8	10	6	ABP71119	Abp71119 E10 prote
45	26	57.8	10	7	ADW30865	Adw30865 HLA bindi

ALIGNMENTS

RESULT 1
AAW99196
ID AAW99196 standard; peptide; 9 AA.
XX
AC AAW99196;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

```
  Query Match             100.0%;  Score 45;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 2
AAW97375
ID   AAW97375 standard; protein; 9 AA.
XX
AC   AAW97375;
XX
DT   13-MAY-1999  (first entry)
XX
DE   HA-1 H-allele sequence.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Claim 18; Fig 5; 59pp; English.
XX
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 H-allele. The specification describes methods for typing
CC   alleles (preferably the H and R alleles) of the minor histocompatibility
CC   antigen HA-1 in a sample, which comprise detecting polymorphic
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 3
ADH40333
ID   ADH40333 standard; peptide; 9 AA.
XX
AC   ADH40333;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 4
AAW99199
ID   AAW99199 standard; peptide; 13 AA.
XX
AC   AAW99199;
XX
DT   20-MAY-1999  (first entry)
XX
DE   vR cell KIAA0223 protein sequence.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
```

XX
OS Synthetic.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
DR N-PSDB; AAX19409.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 31; 47pp; English.
XX
CC The present invention describes a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases. The present sequence represents a KIAA0223 sequence given in
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 3 VLHDDLLEA 11

RESULT 5
AAW97415
ID AAW97415 standard; protein; 13 AA.
XX
AC AAW97415;
XX
DT 20-MAY-1999 (first entry)
XX
DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
OS Homo sapiens.
XX
PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
DR N-PSDB; AAX16081.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Disclosure; Page 38; 57pp; English.
XX
CC The present sequence represents the KIAA0223 polymorphism in HA-1
CC positive homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or Graft-versus-Host
CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 3 VLHDDLLEA 11

RESULT 6
AAW99197
ID AAW99197 standard; peptide; 9 AA.
XX
AC AAW99197;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the

```
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             82.2%;  Score 37;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
AAW97374
ID   AAW97374 standard; protein; 9 AA.
XX
AC   AAW97374;
XX
DT   13-MAY-1999  (first entry)
XX
DE   HA-1 R-allele sequence.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Claim 13; Fig 5; 59pp; English.
XX
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 R-allele. The specification describes methods for typing
CC   alleles (preferably the H and R alleles) of the minor histocompatibility
CC   antigen HA-1 in a sample, which comprise detecting polymorphic
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             82.2%;  Score 37;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 8
ADH40334
ID   ADH40334 standard; peptide; 9 AA.
XX
AC   ADH40334;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             82.2%;  Score 37;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 9
AAW99198
ID   AAW99198 standard; peptide; 13 AA.
XX
AC   AAW99198;
XX
DT   20-MAY-1999  (first entry)
XX
```

```
DE   DH cell KIAA0223 protein sequence.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Synthetic.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
DR   N-PSDB; AAX19408.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Disclosure; Page 31; 47pp; English.
XX
CC   The present invention describes a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases. The present sequence represents a KIAA0223 sequence given in
CC   the present invention
XX
SQ   Sequence 13 AA;

  Query Match             82.2%;  Score 37;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          3 VLRDDLLEA 11


RESULT 10
AAW97414
ID   AAW97414 standard; protein; 13 AA.
XX
AC   AAW97414;
XX
DT   20-MAY-1999  (first entry)
XX
DE   KIAA0223 polymorphism in HA-1 negative homozygous individuals.
XX
KW   T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW   transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW   neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
OS   Homo sapiens.
XX
PN   WO9905173-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000424.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-142855/12.
DR   N-PSDB; AAX16080.
XX
PT   Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT   for inducing tolerance to transplants and prevent rejection or graft-
PT   versus-host disease.
XX
PS   Disclosure; Page 38; 57pp; English.
XX
CC   The present sequence represents the KIAA0223 polymorphism in HA-1
CC   negative homozygous individuals. The specification describes an
CC   immunogenic peptide constituting a T-cell epitope, obtainable from the
CC   minor histocompatibility antigen HA-1. The peptide can be used in
CC   vaccines or pharmaceutical formulations as medicines to induce tolerance
CC   for transplants so as to prevent rejection and/or Graft-versus-Host
CC   Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC   presenting the peptides, in an HLA class I context, can be eliminated
CC   after specific recognition of the peptides. The peptides can also be used
CC   to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ   Sequence 13 AA;

  Query Match             82.2%;  Score 37;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          3 VLRDDLLEA 11


RESULT 11
AAW99195
ID   AAW99195 standard; peptide; 9 AA.
XX
AC   AAW99195;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /label= His, Arg
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
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```
PT   marrow and organ transplantation.
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             80.0%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 12
AAW97572
ID   AAW97572 standard; peptide; 9 AA.
XX
AC   AAW97572;
XX
DT   20-MAY-1999  (first entry)
XX
DE   T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW   T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW   transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW   neoplastic haematopoietic cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /note= "His or Arg"
XX
PN   WO9905173-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000424.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-142855/12.
XX
PT   Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT   for inducing tolerance to transplants and prevent rejection or graft-
PT   versus-host disease.
XX
PS   Claim 1; Page 39; 57pp; English.
XX
CC   The present sequence represents an immunogenic peptide constituting a T-
CC   cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC   The peptide can be used in vaccines or pharmaceutical formulations as
CC   medicines to induce tolerance for transplants so as to prevent rejection
CC   and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC   Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC   I context, can be eliminated after specific recognition of the peptides.
CC   The peptides can also be used to raise antibodies, T-cell receptor, B-
CC   and T-cells
XX
SQ   Sequence 9 AA;

  Query Match             80.0%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 13
ADU99853
ID   ADU99853 standard; peptide; 9 AA.
XX
AC   ADU99853;
XX
DT   24-FEB-2005  (first entry)
XX
DE   BCZ4 tumor antigen antigenic peptide #85.
XX
KW   expression vector; tumor antigen; cancer; cytostatic; BCZ4;
KW   antigenic peptide.
XX
OS   Unidentified.
XX
PN   WO2004104039-A2.
XX
PD   02-DEC-2004.
XX
PF   15-MAY-2004; 2004WO-US015202.
XX
PR   16-MAY-2003; 2003US-0471119P.
PR   16-MAY-2003; 2003US-0471193P.
XX
PA   (AVET ) AVENTIS PASTEUR INC.
XX
PI   Berinstein N,  Gallichan S,  Lovitt C,  Parrington M,  Radvanyi L;
PI   Singh-Sandhu D;
XX
DR   WPI; 2004-834272/82.
XX
PT   New expression vector comprising a nucleic acid encoding a tumor antigen,
PT   e.g. BFA4, BCY1, BFA5, BCZ4, or BFY3, useful for expressing multiple
PT   tumor antigens, or for preventing or treating cancer.
XX
PS   Example 8; Page 60; 109pp; English.
XX
CC   The invention comprises an expression vector that contains a nucleic acid
CC   encoding a tumor antigen (e.g. BCZ4 or BFY3). The expression vector of
CC   the invention is useful for the expression of multiple tumor antigens and
CC   the prevention or treatment of cancer. The present amino acid sequence
CC   represents a BCZ4 tumor antigen antigenic peptide that was used in an
CC   example of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             68.9%;  Score 31;  DB 8;  Length 9;
  Best Local Similarity   85.7%;  Pred. No. 2e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              || ||||
Db          2 LHSDLLE 8


RESULT 14
AAW97373
ID   AAW97373 standard; peptide; 9 AA.
XX
AC   AAW97373;
XX
```

```
DT   13-MAY-1999  (first entry)
XX
DE   Peptide epitope of HA-1 antigen.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "not specified"
FT   Misc-difference 6
FT                   /note= "not specified"
FT   Misc-difference 7
FT                   /note= "not specified"
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Example 1; Page 22; 59pp; English.
XX
CC   The present sequence represents an epitope of the minor
CC   histocompatibility antigen HA-1. The specification describes methods for
CC   typing alleles (preferably the H and R alleles) of the minor
CC   histocompatibility antigen HA-1 in a sample, which comprise detecting
CC   polymorphic nucleotides in the cDNA or genomic nucleic acids of the
CC   alleles. The methods can be used for HA-1 typing for bone marrow
CC   transplants, severe aplastic anaemia, leukaemia and immune deficiency
CC   diseases, as well as detection of genetic aberrances. The probes and
CC   primers of the invention can be used to screen for the HA-1 alleles. The
CC   HA-1 peptides can be used anti-idiotypic B cells and/or T cells and
CC   antibodies
XX
SQ   Sequence 9 AA;

  Query Match             66.7%;  Score 30;  DB 2;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              | |||  ||
Db          1 VXHDDXXEA 9


RESULT 15
AAU02706
ID   AAU02706 standard; peptide; 13 AA.
XX
AC   AAU02706;
XX
DT   29-AUG-2001  (first entry)
XX
DE   CDR region of anti-adipocyte antibody heavy chain, FAT 71.
XX
KW   Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW   heart disease; complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   WO200127279-A1.
XX
PD   19-APR-2001.
XX
PF   11-OCT-2000; 2000WO-GB003900.
XX
PR   12-OCT-1999;   99US-0158812P.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Edwards BM,  Main SH,  Vaughan TJ;
XX
DR   WPI; 2001-282031/29.
DR   N-PSDB; AAS03483.
XX
PT   Panel of specific binding members of antibody molecules which bind to
PT   whole adipocytes is used in the treatment of obesity and obesity related
PT   diseases.
XX
PS   Example 7; Page 78; 182pp; English.
XX
CC   AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC   sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC   and heavy chain complementarity determining regions (CDR) of the
CC   invention. The antibodies can be used in the treatment of obesity and
CC   obesity related diseases. The antibodies can be used to deliver drugs or
CC   pro-drugs directly to the fat mass of an obese patient or the antibody
CC   can be used as a therapeutic itself. Antibodies binding specifically to
CC   adipocytes can be used to activate the immune system to destroy the cells
CC   by complement mediated lysis. The antibodies may be labeled with a
CC   detectable label such as radiolabel, fluorescent or chemical group and
CC   used in methods of diagnosis in human subjects e.g. to determine the
CC   presence of adipocyte antigen on the surface of an adipocyte to detect or
CC   determine the presence or level of adipocytes in a cell or tissue sample.
CC   The antibodies can be used as an alternative means of treatment for obese
CC   patients other than undergoing surgery to remove excess fat. Antibodies
CC   for different types of fat deposits can also be produced e.g. intra-
CC   abdominal fat associated with heart disease
XX
SQ   Sequence 13 AA;

  Query Match             64.4%;  Score 29;  DB 4;  Length 13;
  Best Local Similarity   62.5%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLE 8
              |:|||  |
Db          5 VVHDDAFE 12


Search completed: April  6, 2006, 16:57:03
Job time : 115 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:57:26 ; Search time 19 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	46.7	15	2	A53594	calnexin - mouse (
2	19	42.2	15	2	S30608	translation elonga
3	19	42.2	15	2	A45096	thyrotropin-releas
4	18	40.0	7	2	I46868	alpha-myosin heavy
5	18	40.0	10	2	B59272	peptide-N4-(N-acet
6	18	40.0	10	2	C26997	unspecific monooxy
7	18	40.0	15	2	S29485	GTP-binding protei
8	18	40.0	15	2	E56819	PS I complex subun
9	18	40.0	15	2	A26997	unspecific monooxy
10	17	37.8	9	2	S55696	phosphoenolpyruvat
11	17	37.8	10	2	S13224	virG protein - Agr
12	17	37.8	10	2	S30348	clotting protein -
13	17	37.8	11	2	PH0924	T-cell receptor be
14	17	37.8	12	2	S39762	cytochrome P450 UT
15	17	37.8	13	2	PS0443	potassium channel
16	17	37.8	14	2	S50900	chlorophyll a/b-bi
17	17	37.8	14	2	S74128	superoxide dismuta
18	17	37.8	14	2	C39170	acyl-[acyl-carrier
19	17	37.8	15	2	S62675	collagen type I -
20	16	35.6	7	2	PQ0663	membrane protein -
21	16	35.6	7	2	S68004	hucolin, 75K chain
22	16	35.6	8	2	PC4131	hypothetical prote
23	16	35.6	10	1	SPPGNK	neuromedin K - pig
24	16	35.6	10	2	A61354	carnitine medium/l
25	16	35.6	10	2	F44644	neurotoxin-associa
26	16	35.6	11	2	S78765	ribosomal protein
27	16	35.6	13	2	G44644	neurotoxin-associa
28	16	35.6	13	2	S14316	photosystem I 9K c
29	16	35.6	14	1	LFEBWC	trp operon leader
30	16	35.6	14	2	S29789	hypothetical prote
31	16	35.6	14	2	S48685	extension protein
32	16	35.6	15	2	S14749	3-dehydroquinase -
33	16	35.6	15	2	B32800	hypothetical prote
34	16	35.6	15	2	B26501	lipoprotein lipase
35	15	33.3	6	2	S78764	ribosomal protein
36	15	33.3	7	2	A59489	protein kinase C i
37	15	33.3	11	2	A14454	6-phosphofructokin
38	15	33.3	11	4	S41909	hypothetical prote
39	15	33.3	13	2	PT0256	Ig heavy chain CRD
40	15	33.3	13	2	S65612	tubulin alpha-chai
41	15	33.3	13	2	S00316	photosystem I 13K
42	15	33.3	14	2	PH1626	Ig H chain V-D-J r
43	15	33.3	14	2	A61306	ribonuclease M (EC
44	15	33.3	15	2	PA0009	seed storage prote
45	15	33.3	15	2	PQ0750	self-incompatibili

ALIGNMENTS

RESULT 1
A53594
calnexin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A53594
R;Lenter, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A;Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin pı
A;Reference number: A53594; MUID:94216347; PMID:8163531
A;Accession: A53594
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <LEN>
A;Cross-references: UNIPROT:Q7M063; UNIPARC:UPI000017C62E
C;Keywords: endoplasmic reticulum; molecular chaperone

Query Match 46.7%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLHDDL 6
              :: |||
Db         10 IIEDDL 15
```

RESULT 2
S30608
translation elongation factor eEF-2 - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 07-May-1999
C;Accession: S30608
R;Brown, B.A.; Bodley, J.W.
FEBS Lett. 103, 253-255, 1979
A;Title: Primary structure at the site in beef and wheat elongation factor 2 of ADP-ribo
A;Reference number: S30607; MUID:79236796; PMID:467667
A;Accession: S30608
A;Molecule type: protein
A;Residues: 1-15 <BRO>
A;Cross-references: UNIPARC:UPI000017482A
A;Experimental source: liver
C;Keywords: GTP binding; protein biosynthesis

Query Match 42.2%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 LHDDLLEA 9
              :||  | |
Db          3 VHDVTLHA 10
```

```
RESULT 3
A45096
thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A45096
R;de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
J. Biol. Chem. 267, 25703-25708, 1992
A;Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alterna
A;Reference number: A45096; MUID:93100278; PMID:1334485
A;Accession: A45096
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-15 <DE1>
A;Cross-references: UNIPARC:UPI0000170C44; GB:S51512; NID:g261982; PIDN:AAB24549.1; PID:
A;Experimental source: GH3 anterior pituitary cells
A;Note: sequence extracted from NCBI backbone (NCBIP:120927)

  Query Match             42.2%;  Score 19;  DB 2;  Length 15;
  Best Local Similarity   42.9%;  Pred. No. 1.7e+03;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLL 7
              ::| |:|
Db          9 LVHMDIL 15


RESULT 4
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: UNIPROT:Q28742; UNIPARC:UPI0000087938; GB:K01698; NID:g165538; PIDN:

  Query Match             40.0%;  Score 18;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDD 5
              :||:
Db          3 MHDE 6


RESULT 5
B59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -
N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: B59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: B59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
A;Cross-references: UNIPROT:P81898; UNIPARC:UPI00000ABBC4
C;Keywords: hydrolase

  Query Match             40.0%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHD 4
              |||
Db          5 LHD 7


RESULT 6
C26997
unspecific monooxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic - ra
N;Alternate names: cytochrome P450
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: C26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A;Reference number: A26997; MUID:88000604; PMID:3651420
A;Accession: C26997
A;Molecule type: protein
A;Residues: 1-10 <GRA>
A;Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA8
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

  Query Match             40.0%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              ||| |
Db          2 DLLSA 6


RESULT 7
S29485
GTP-binding protein o-ral - Pacific electric ray (fragment)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S29485
R;Volknandt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A;Reference number: S29485; MUID:93154521; PMID:8428634
A;Accession: S29485
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <VOL>
A;Cross-references: UNIPARC:UPI000017BF33

  Query Match             40.0%;  Score 18;  DB 2;  Length 15;
  Best Local Similarity   28.6%;  Pred. No. 2.6e+03;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              ::|: :|
Db          1 MYDEFVE 7


RESULT 8
E56819
PS I complex subunit 8 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: E56819
R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-t
A;Reference number: A56819; MUID:91355209; PMID:1883835
A;Accession: E56819
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <IWA>
A;Cross-references: UNIPROT:P42052; UNIPARC:UPI0000132593
```

```
A;Note: sequence extracted from NCBI backbone (NCBIP:58606)

  Query Match             40.0%;  Score 18;  DB 2;  Length 15;
  Best Local Similarity   60.0%;  Pred. No. 2.6e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              |: ||
Db         10 VIQDD 14


RESULT 9
A26997
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
N;Alternate names: cytochrome P450b
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: A26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A;Reference number: A26997; MUID:88000604; PMID:3651420
A;Accession: A26997
A;Molecule type: protein
A;Residues: 1-15 <GRA>
A;Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA7
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

  Query Match             40.0%;  Score 18;  DB 2;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              ||| |
Db          2 DLLSA 6


RESULT 10
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55696
R;Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try
A;Reference number: S55696; MUID:95284106; PMID:7766679
A;Accession: S55696
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <HUN>
A;Cross-references: UNIPROT:Q7M3S5; UNIPARC:UPI000017B599

  Query Match             37.8%;  Score 17;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::| :|
Db          3 IIHKNL 8


RESULT 11
S13224
virG protein - Agrobacterium sp. (fragment)
C;Species: Agrobacterium sp.
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S13224
R;Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.
J. Mol. Biol. 215, 537-547, 1990
A;Title: Binding of the regulatory protein VirG to the phased signal sequences upstream
A;Reference number: S13224; MUID:91039316; PMID:2231718
A;Accession: S13224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAM>
A;Cross-references: UNIPROT:Q7M0P7; UNIPARC:UPI000017A9C4

  Query Match             37.8%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 2.5e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              |: ||
Db          6 VIDDD 10


RESULT 12
S30348
clotting protein - signal crayfish
C;Species: Pacifastacus leniusculus (signal crayfish)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S30348
R;Kopacek, P.; Hall, M.; Soederhaell, K.
Eur. J. Biochem. 213, 591-597, 1993
A;Title: Characterization of a clotting protein, isolated from plasma of the freshwater
A;Reference number: S30348; MUID:93238739; PMID:8097463
A;Accession: S30348
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <KOP>
A;Cross-references: UNIPROT:P81070; UNIPROT:Q9UAR3; UNIPARC:UPI000017BDEA

  Query Match             37.8%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 2.5e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              || :|
Db          1 LHSNL 5


RESULT 13
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Cross-references: UNIPARC:UPI000017C9F3
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

  Query Match             37.8%;  Score 17;  DB 2;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              ||:|
Db          7 DLME 10


RESULT 14
S39762
cytochrome P450 UT-7b - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S39762
R;Ohishi, N.; Imaoka, S.; Suzuki, T.; Funae, Y.
```

Biochim. Biophys. Acta 1158, 227-236, 1993
A;Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
A;Reference number: S39761; MUID:94072607; PMID:8251521
A;Accession: S39762
A;Molecule type: protein
A;Residues: 1-12 <OHI>
A;Cross-references: UNIPARC:UPI000017C8F7

Query Match 37.8%; Score 17; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDL 6
:: |||
Db 3 LIGDDL 8

RESULT 15
PS0443
potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C;Accession: PS0443
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A;Reference number: JH0697; MUID:92360298; PMID:1497890
A;Accession: PS0443
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-13 <ADE>
A;Cross-references: UNIPARC:UPI000017BEBA
C;Comment: This potassium channel is activated by calcium.
C;Genetics:
A;Gene: FlyBase:slo
A;Cross-references: FlyBase:FBgn0003429
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 37.8%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLL 7
|||:
Db 10 DDLV 13

Search completed: April 6, 2006, 17:04:00
Job time : 20 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:51:26 ; Search time 116.333 Seconds
(without alignments)
54.582 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	48.9	12	2	Q6LAP7_HUMAN	Q6lap7 homo sapien
2	22	48.9	13	2	Q6LCH4_RAT	Q6lch4 rattus norv
3	22	48.9	14	2	O95179_HUMAN	O95179 homo sapien
4	22	48.9	15	2	Q86TJ6_HUMAN	Q86tj6 homo sapien
5	22	48.9	15	2	Q9TWT4_LUMTE	Q9twt4 lumbricus t
6	21	46.7	11	1	UF05_MOUSE	P38643 mus musculu
7	21	46.7	11	2	Q66874_9CALI	Q66874 feline cali
8	21	46.7	11	2	Q66877_9CALI	Q66877 feline cali
9	21	46.7	15	2	Q7M063_MOUSE	Q7m063 mus musculu
10	20	44.4	10	1	FIBB_CERSI	P14537 ceratotheri
11	20	44.4	11	2	Q47600_ECOLI	Q47600 escherichia
12	20	44.4	12	1	XYLA_STRVN	P14405 streptomyce
13	20	44.4	15	2	Q9R5D6_CHRVI	Q9r5d6 chromatium
14	19	42.2	9	2	Q7R8X5_PLAYO	Q7r8x5 plasmodium
15	19	42.2	9	2	Q47556_ECOLI	Q47556 escherichia
16	19	42.2	11	2	Q6LBJ0_MOUSE	Q6lbj0 mus musculu
17	19	42.2	13	2	P82560_STRPY	P82560 streptococc
18	19	42.2	14	2	Q9ZB42_STRPY	Q9zb42 streptococc
19	18	40.0	7	2	Q28742_RABIT	Q28742 oryctolagus
20	18	40.0	10	2	Q718N9_9PARA	Q718n9 newcastle d
21	18	40.0	11	2	Q718K6_9PARA	Q718k6 newcastle d
22	18	40.0	12	1	LICA_BACSU	P83878 bacillus su
23	18	40.0	12	1	LICB_BACSU	P83879 bacillus su
24	18	40.0	12	1	LICH_BACLI	P82907 bacillus li
25	18	40.0	12	2	Q9T2U3_BOVIN	Q9t2u3 bos taurus
26	18	40.0	12	2	Q9TQY4_BOVIN	Q9tqy4 bos taurus
27	18	40.0	12	2	Q5MK49_9CLOS	Q5mk49 citrus tris
28	18	40.0	12	2	Q5MK52_9CLOS	Q5mk52 citrus tris
29	18	40.0	12	2	Q5MK66_9CLOS	Q5mk66 citrus tris
30	18	40.0	12	2	Q5MK81_9CLOS	Q5mk81 citrus tris
31	18	40.0	13	2	Q7YRD1_BISBO	Q7yrd1 bison bonas
32	18	40.0	13	2	Q7YRI4_BOVIN	Q7yri4 bos taurus
33	18	40.0	13	2	Q7TE19_9CLOS	Q7te19 citrus tris
34	18	40.0	13	2	Q7TE20_9CLOS	Q7te20 citrus tris
35	18	40.0	13	2	Q7TE23_9CLOS	Q7te23 citrus tris
36	18	40.0	13	2	Q7TE26_9CLOS	Q7te26 citrus tris
37	18	40.0	13	2	Q7TE30_9CLOS	Q7te30 citrus tris
38	18	40.0	13	2	Q957T7_9PERC	Q957t7 trichopsis
39	18	40.0	14	1	SODN_STRGR	P80732 streptomyce
40	18	40.0	14	2	Q8HR43_CLIMI	Q8hr43 clivia mini
41	18	40.0	14	2	Q52840_RHILO	Q52840 rhizobium l
42	18	40.0	15	1	PSAO_CUCSA	P42052 cucumis sat
43	18	40.0	15	2	Q9UC60_HUMAN	Q9uc60 homo sapien
44	17	37.8	9	2	Q7M3S5_9TRYP	Q7m3s5 trypanosoma
45	17	37.8	10	2	Q9UWM5_SULSO	Q9uwm5 sulfolobus

ALIGNMENTS

RESULT 1
Q6LAP7_HUMAN
ID Q6LAP7_HUMAN PRELIMINARY; PRT; 12 AA.
AC Q6LAP7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glucose-6-phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96184388; PubMed=8612793; DOI=10.1016/0014-5793(96)00224-4;
RA Schmoll D., Allan B.B., Burchell A.;
RT "Cloning and sequencing of the 5 region of the human glucose-6-
RT phosphatase gene: transcriptional regulation by cAMP, insulin and
RT glucocorticoids in H411E hepatoma cells.";
RL FEBS Lett. 383:63-66(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Allan Brian B.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X96937; CAA65638.1; -; Genomic_DNA.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1379 MW; A6B78EEFDE32C446 CRC64;

Query Match 48.9%; Score 22; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 VLHD 4
              ||||
Db          7 VLHD 10
```

RESULT 2
Q6LCH4_RAT
ID Q6LCH4_RAT PRELIMINARY; PRT; 13 AA.
AC Q6LCH4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glucose-6-phosphatase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;

```
RX   MEDLINE=97020177; PubMed=8866562;
RA   Argaud D., Zhang Q., Pan W., Maitra S., Pilkis S.J., Lange A.J.;
RT   "Regulation of rat liver glucose-6-phosphatase gene expression in
RT   different nutritional and hormonal states: gene structure and 5'-
RT   flanking sequence.";
RL   Diabetes 45:1563-1571(1996).
DR   EMBL; U57552; AAB19044.1; -; Genomic_DNA.
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1591 MW;  0926B68EEFDE32C4 CRC64;

  Query Match             48.9%;  Score 22;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHD 4
              ||||
Db          7 VLHD 10


RESULT 3
O95179_HUMAN
ID   O95179_HUMAN PRELIMINARY;      PRT;    14 AA.
AC   O95179;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Glucose-6-phosphatase hydrolytic subunit (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99156747; PubMed=10024523; DOI=10.1042/0264-6021:3380457;
RA   Schmoll D., Wasner C., Hinds C.J., Allan B.B., Walther R.,
RA   Burchell A.;
RT   "Identification of a cAMP response element within the glucose- 6-
RT   phosphatase hydrolytic subunit gene promoter which is involved in the
RT   transcriptional regulation by cAMP and glucocorticoids in H4IIE
RT   hepatoma cells.";
RL   Biochem. J. 338:457-463(1999).
DR   EMBL; AF051355; AAD11621.1; -; Genomic_DNA.
FT   NON_TER      14     14
SQ   SEQUENCE   14 AA;  1666 MW;  A6B78EEF99F7FD46 CRC64;

  Query Match             48.9%;  Score 22;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHD 4
              ||||
Db          9 VLHD 12


RESULT 4
Q86TJ6_HUMAN
ID   Q86TJ6_HUMAN PRELIMINARY;      PRT;    15 AA.
AC   Q86TJ6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   FLJ20097 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC047757; AAH47757.1; -; mRNA.
SQ   SEQUENCE   15 AA;  1843 MW;  C309CDBA5B044A3F CRC64;

  Query Match             48.9%;  Score 22;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHD 4
              ||||
Db         12 VLHD 15


RESULT 5
Q9TWT4_LUMTE
ID   Q9TWT4_LUMTE  PRELIMINARY;      PRT;    15 AA.
AC   Q9TWT4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Hemoglobin (Fragment).
OS   Lumbricus terrestris (Common earthworm).
OC   Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC   Lumbricina; Lumbricidae; Lumbricus.
OX   NCBI_TaxID=6398;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93293879; PubMed=8514787;
RA   Ownby D.W., Zhu H., Schneider K., Beavis R.C., Chait B.T., Riggs A.F.;
RT   "The extracellular hemoglobin of the earthworm, Lumbricus terrestris.
RT   Determination of subunit stoichiometry.";
RL   J. Biol. Chem. 268:13539-13547(1993).
SQ   SEQUENCE   15 AA;  1665 MW;  F9B83FE0050D91F5 CRC64;

  Query Match             48.9%;  Score 22;  DB 2;  Length 15;
  Best Local Similarity   33.3%;  Pred. No. 3.8e+03;
  Matches    2;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HDDLLE 8
              ||::::
Db          8 HDEIID 13


RESULT 6
UF05_MOUSE
ID   UF05_MOUSE     STANDARD;      PRT;    11 AA.
AC   P38643;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
```

```
DE   Unknown protein from 2D-PAGE of fibroblasts (P48) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins using
RT   preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 5.5, its MW is: 48 kDa.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   Direct protein sequencing.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1330 MW;  E54835E5CAAABAFA CRC64;

  Query Match             46.7%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   37.5%;  Pred. No. 4.2e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLE 8
              :  ||::|
Db          3 IXXDDVIE 10


RESULT 7
Q66874_9CALI
ID   Q66874_9CALI PRELIMINARY;      PRT;    11 AA.
AC   Q66874;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Polymerase (Fragment).
OS   Feline calicivirus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC   Vesivirus.
OX   NCBI_TaxID=11978;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=255;
RX   MEDLINE=95250311; PubMed=7732664;
RA   Seal B.S., Neill J.D.;
RT   "Capsid protein gene sequence of feline calicivirus isolates 255 and
RT   LLK: further evidence for capsid protein configuration among feline
RT   caliciviruses.";
RL   Virus Genes 9:183-187(1995).
DR   EMBL; U07130; AAA74412.1; -; Genomic_RNA.
FT   NON_TER      1      1
SQ   SEQUENCE   11 AA;  1232 MW;  4E8E5F5CCAAEB1E7 CRC64;

  Query Match             46.7%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 4.2e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              || |: |
Db          4 LHCDVFE 10


RESULT 8
Q66877_9CALI
ID   Q66877_9CALI PRELIMINARY;      PRT;    11 AA.
AC   Q66877;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Polymerase (Fragment).
OS   Feline calicivirus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC   Vesivirus.
OX   NCBI_TaxID=11978;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=LLK;
RX   MEDLINE=95250311; PubMed=7732664;
RA   Seal B.S., Neill J.D.;
RT   "Capsid protein gene sequence of feline calicivirus isolates 255 and
RT   LLK: further evidence for capsid protein configuration among feline
RT   caliciviruses.";
RL   Virus Genes 9:183-187(1995).
DR   EMBL; U07131; AAA74415.1; -; Genomic_RNA.
FT   NON_TER      1      1
SQ   SEQUENCE   11 AA;  1264 MW;  5E9F43EBCAAEB1E7 CRC64;

  Query Match             46.7%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 4.2e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              || |: |
Db          4 LHCDVFE 10


RESULT 9
Q7M063_MOUSE
ID   Q7M063_MOUSE PRELIMINARY;      PRT;    15 AA.
AC   Q7M063;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Calnexin (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=94216347; PubMed=8163531;
RA   Lenter M., Vestweber D.;
RT   "The integrin chains beta-1 and alpha-6 associate with the chaperone
RT   calnexin prior to integrin assembly.";
RL   J. Biol. Chem. 269:12263-12268(1994).
DR   PIR; A53594; A53594.
FT   NON_TER      1      1
FT   NON_TER     15     15
SQ   SEQUENCE   15 AA;  1693 MW;  C62AAAA42F9F5F35 CRC64;

  Query Match             46.7%;  Score 21;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 5.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              :: |||
Db         10 IIEDDL 15


RESULT 10
FIBB_CERSI
ID   FIBB_CERSI     STANDARD;      PRT;    10 AA.
AC   P14537;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   01-FEB-2005 (Rel. 46, Last annotation update)
DE   Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
```

```
GN   Name=FGB;
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Rhinocerotidae;
OC   Ceratotherium.
OX   NCBI_TaxID=9807;
RN   [1]
RP   PROTEIN SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC       nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC       are in head to head conformation with the N-termini in a small
CC       central domain (By similarity).
CC   -!- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC       chains connects the central nodule to the C-terminal domains
CC       (distal nodules). The long C-terminal ends of the alpha chains
CC       fold back, contributing a fourth strand to the coiled coil
CC       structure.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   InterPro; IPR002181; Fibrinogen_C.
DR   PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW   Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
FT   PEPTIDE       1     10       Fibrinopeptide B.
FT   NON_TER       10    10
SQ   SEQUENCE   10 AA;  1097 MW;  9402B2B2CDDDD33A CRC64;

  Query Match             44.4%;  Score 20;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HDD 5
              |||
Db          1 HDD 3


RESULT 11
Q47600_ECOLI
ID   Q47600_ECOLI PRELIMINARY;      PRT;    11 AA.
AC   Q47600;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   REase protein (Fragment).
GN   Name=REase;
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91139577; PubMed=1995588;
RA   Tao T., Bourne J.C., Blumenthal R.M.;
RT   "A family of regulatory genes associated with type II restriction-
RT   modification systems.";
RL   J. Bacteriol. 173:1367-1375(1991).
DR   EMBL; M63619; AAA24556.1; -; Genomic_DNA.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1232 MW;  63175479572AB5A4 CRC64;

  Query Match             44.4%;  Score 20;  DB 2;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 6.6e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 LHDDLLEA 9
              |  ||: |
Db          3 LRSDLINA 10


RESULT 12
XYLA_STRVN
ID   XYLA_STRVN     STANDARD;      PRT;    12 AA.
AC   P14405;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Xylose isomerase (EC 5.3.1.5) (Fragment).
GN   Name=xylA;
OS   Streptomyces violaceoruber.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1935;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   STRAIN=LMG 7183;
RX   MEDLINE=90104230; PubMed=2604694;
RA   Vangrysperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
RT   "Single active-site histidine in D-xylose isomerase from Streptomyces
RT   violaceoruber. Identification by chemical derivatization and peptide
RT   mapping.";
RL   Biochem. J. 263:195-199(1989).
CC   -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC   -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC   -!- SUBUNIT: Homotetramer.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the xylose isomerase family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   HAMAP; MF_00455; -; 1.
DR   InterPro; IPR001998; Xylose_isom.
DR   PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR   PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW   Carbohydrate metabolism; Direct protein sequencing; Isomerase;
KW   Magnesium; Metal-binding; Pentose shunt; Xylose metabolism.
FT   ACT_SITE      5      5
FT   ACT_SITE      8      8       By similarity.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1376 MW;  E749268EB1AAAAA1 CRC64;

  Query Match             44.4%;  Score 20;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HDD 5
              |||
Db          5 HDD 7


RESULT 13
Q9R5D6_CHRVI
ID   Q9R5D6_CHRVI  PRELIMINARY;      PRT;    15 AA.
AC   Q9R5D6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein
```

```
DE   (Fragment).
OS   Chromatium vinosum.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC   Chromatiaceae; Allochromatium.
OX   NCBI_TaxID=1049;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93146381; PubMed=1490603; DOI=10.1016/0378-1097(92)90031-I;
RA   Liebergesell M., Schmidt B., Steinbuchel A.;
RT   "Isolation and identification of granule-associated proteins relevant
RT   for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
RT   D.";
RL   FEMS Microbiol. Lett. 78:227-232(1992).
SQ   SEQUENCE   15 AA;  1874 MW;  165FA9A16BCA2A9D CRC64;

  Query Match             44.4%;  Score 20;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 9.2e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HDDLLE 8
              :|| ||
Db          8 NDDWLE 13


RESULT 14
Q7R8X5_PLAYO
ID   Q7R8X5_PLAYO PRELIMINARY;      PRT;     9 AA.
AC   Q7R8X5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=PY07095;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=17XNL;
RX   MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01002528; EAA19452.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   9 AA;  1013 MW;  4684D447244441E7 CRC64;

  Query Match             42.2%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              :|||:|
Db          1 MLHNNL 6


RESULT 15
Q47556_ECOLI
ID   Q47556_ECOLI PRELIMINARY;      PRT;     9 AA.
AC   Q47556;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Aspartate transcarbamoylase regulatory chain (Fragment).
GN   Name=pyrI;
OS   Escherichia coli K12.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83333;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82275057; PubMed=7051000;
RA   Pauza C.D., Karels M.J., Navre M., Schachman H.K.;
RT   "Genes encoding Escherichia coli aspartate transcarbamoylase: the
RT   pyrB-pyrI operon.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83195078; PubMed=6302686;
RA   Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
RA   Wild J.R.;
RT   "Nucleotide sequence of the structural gene (pyrB) that encodes the
RT   catalytic polypeptide of aspartate transcarbamoylase of Escherichia
RT   coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
DR   EMBL; J01670; AAA24475.1; -; Genomic_DNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1085 MW;  99EFD723344AA1F1 CRC64;

  Query Match             42.2%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HDDLLE 8
              ||: |:
Db          3 HDNKLQ 8


Search completed: April  6, 2006, 17:02:58
Job time : 117.333 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:03:16 ; Search time 27.6667 Seconds
(without alignments)
26.894 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	2	US-09-269-250E-20	Sequence 20, Appl
2	45	100.0	9	2	US-09-489-760-2	Sequence 2, Appli
3	45	100.0	13	2	US-09-269-250E-28	Sequence 28, Appl
4	45	100.0	13	2	US-09-489-760-16	Sequence 16, Appl
5	37	82.2	9	2	US-09-269-250E-18	Sequence 18, Appl
6	37	82.2	9	2	US-09-489-760-5	Sequence 5, Appli
7	37	82.2	13	2	US-09-269-250E-26	Sequence 26, Appl
8	37	82.2	13	2	US-09-489-760-14	Sequence 14, Appl
9	36	80.0	9	2	US-09-269-250E-29	Sequence 29, Appl
10	36	80.0	9	2	US-09-489-760-1	Sequence 1, Appli
11	30	66.7	9	2	US-09-489-760-4	Sequence 4, Appli
12	28.5	63.3	8	2	US-09-269-250E-38	Sequence 38, Appl
13	25	55.6	7	2	US-09-025-819-5	Sequence 5, Appli
14	25	55.6	7	2	US-09-808-126-5	Sequence 5, Appli
15	25	55.6	7	2	US-09-803-951-5	Sequence 5, Appli
16	25	55.6	9	2	US-08-582-333A-3	Sequence 3, Appli
17	25	55.6	9	2	US-09-305-923A-7	Sequence 7, Appli
18	25	55.6	9	2	US-08-946-298-4	Sequence 4, Appli
19	24	53.3	10	1	US-08-724-548-20	Sequence 20, Appl
20	24	53.3	10	1	US-08-724-548-21	Sequence 21, Appl
21	24	53.3	10	1	US-08-724-548-22	Sequence 22, Appl
22	24	53.3	10	1	US-08-724-548-23	Sequence 23, Appl
23	24	53.3	10	1	US-08-724-548-24	Sequence 24, Appl
24	24	53.3	10	1	US-08-724-548-25	Sequence 25, Appl
25	24	53.3	10	1	US-08-724-548-26	Sequence 26, Appl
26	24	53.3	10	2	US-08-159-339A-73	Sequence 73, Appl
27	24	53.3	10	2	US-07-978-674B-20	Sequence 20, Appl
28	24	53.3	10	2	US-07-978-674B-21	Sequence 21, Appl
29	24	53.3	10	2	US-07-978-674B-22	Sequence 22, Appl
30	24	53.3	10	2	US-07-978-674B-23	Sequence 23, Appl
31	24	53.3	10	2	US-07-978-674B-24	Sequence 24, Appl
32	24	53.3	10	2	US-07-978-674B-25	Sequence 25, Appl
33	24	53.3	10	2	US-07-978-674B-26	Sequence 26, Appl
34	24	53.3	10	2	US-08-197-484-72	Sequence 72, Appl
35	24	53.3	10	2	US-09-601-729-273	Sequence 273, App
36	24	53.3	10	4	PCT-US95-02121-72	Sequence 72, Appl
37	24	53.3	14	1	US-07-909-122-3	Sequence 3, Appli
38	23	51.1	6	2	US-09-217-609A-8	Sequence 8, Appli
39	23	51.1	6	2	US-08-873-235B-8	Sequence 8, Appli
40	23	51.1	9	2	US-08-159-339A-370	Sequence 370, App
41	23	51.1	10	2	US-10-121-857-1	Sequence 1, Appli
42	23	51.1	10	2	US-10-121-857-14	Sequence 14, Appl
43	23	51.1	11	2	US-09-489-156-47	Sequence 47, Appl
44	23	51.1	12	1	US-08-360-784B-32	Sequence 32, Appl
45	23	51.1	12	2	US-09-054-308A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen

US-09-489-760-2

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 1 VLHDDLLEA 9

RESULT 3
US-09-269-250E-28
; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 3 VLHDDLLEA 11

RESULT 4
US-09-489-760-16
; Sequence 16, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:HA-1+/+
US-09-489-760-16

Query Match 100.0%; Score 45; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 3 VLHDDLLEA 11

RESULT 5
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 6
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 7
US-09-269-250E-26
; Sequence 26, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-26

  Query Match             82.2%;  Score 37;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 1.1;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          3 VLRDDLLEA 11


RESULT 8
US-09-489-760-14
; Sequence 14, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:HA-1-/-
US-09-489-760-14

  Query Match             82.2%;  Score 37;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 1.1;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          3 VLRDDLLEA 11


RESULT 9
US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

  Query Match             80.0%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 10
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
;   OTHER INFORMATION: RESIDUE
US-09-489-760-1

  Query Match             80.0%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 11
US-09-489-760-4
; Sequence 4, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (2)..(7)
;   OTHER INFORMATION: AMINO ACIDS X REPRESENT LEUCINE OR ISOLEUCINE
;   OTHER INFORMATION: RESIDUES
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US-09-489-760-4

Query Match 66.7%; Score 30; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 VLHDDLLEA 9
              | |||  ||
Db          1 VXHDDXXEA 9
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RESULT 12
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
US-09-269-250E-38

Query Match 63.3%; Score 28.5; DB 2; Length 8;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 VLHDDLLEA 9
              ||| |||||
Db          1 VLH-DLLEA 8
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RESULT 13
US-09-025-819-5
; Sequence 5, Application US/09025819
; Patent No. 6225097
; GENERAL INFORMATION:
; APPLICANT: Obata, Shusei
; APPLICANT: Nishino, Tokuzo
; APPLICANT: Koyama, Tanetoshi
; APPLICANT: Sato, Yoshihiro
; TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KENYON & KENYON
; STREET: 1500 K Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,819
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 251675
; FILING DATE: 17-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Khalilian, Houri
; REGISTRATION NUMBER: 39,546
; REFERENCE/DOCKET NUMBER: 10235/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-220-4200
; TELEFAX: 202-220-4201
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-819-5

Query Match 55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VLHDD 5
              :||||
Db          3 LLHDD 7
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RESULT 14
US-09-808-126-5
; Sequence 5, Application US/09808126
; Patent No. 6410280
; GENERAL INFORMATION:
; APPLICANT: Obata, Shusei
; Nishino, Tokuzo
; Koyama, Tanetoshi
; Sato, Yoshihiro
; TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KENYON & KENYON
; STREET: 1500 K Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/808,126
; FILING DATE: 08-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,819
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Khalilian, Houri
; REGISTRATION NUMBER: 39,546
; REFERENCE/DOCKET NUMBER: 10235/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-220-4200
; TELEFAX: 202-220-4201
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-808-126-5

Query Match 55.6%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VLHDD 5
              :||||
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Db          3 LLHDD 7


RESULT 15
US-09-803-951-5
; Sequence 5, Application US/09803951
; Patent No. 6413761
;   GENERAL INFORMATION:
;        APPLICANT: Obata, Shusei
;                   Nishino, Tokuzo
;                   Koyama, Tanetoshi
;                   Sato, Yoshihiro
;        TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KENYON & KENYON
;             STREET: 1500 K Street, N.W.
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/803,951
;             FILING DATE: 13-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/025,819
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Khalilian, Houri
;             REGISTRATION NUMBER: 39,546
;             REFERENCE/DOCKET NUMBER: 10235/2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-220-4200
;             TELEFAX: 202-220-4201
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-803-951-5

  Query Match             55.6%;  Score 25;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              :||||
Db          3 LLHDD 7


Search completed: April  6, 2006, 17:05:28
Job time : 27.6667 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:22:22 ; Search time 96.6667 Seconds
(without alignments)
38.901 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	4	US-10-623-176-2	Sequence 2, Appli
2	45	100.0	9	4	US-10-791-217-2	Sequence 2, Appli
3	45	100.0	9	5	US-10-861-335-1	Sequence 1, Appli
4	45	100.0	9	6	US-11-007-740-20	Sequence 20, Appl
5	45	100.0	10	4	US-10-623-176-43	Sequence 43, Appl
6	45	100.0	13	4	US-10-623-176-76	Sequence 76, Appl
7	45	100.0	13	4	US-10-791-217-16	Sequence 16, Appl
8	45	100.0	13	6	US-11-007-740-28	Sequence 28, Appl
9	41	91.1	9	4	US-10-623-176-41	Sequence 41, Appl
10	41	91.1	9	4	US-10-623-176-45	Sequence 45, Appl
11	37	82.2	9	4	US-10-623-176-10	Sequence 10, Appl
12	37	82.2	9	4	US-10-623-176-47	Sequence 47, Appl
13	37	82.2	9	4	US-10-791-217-5	Sequence 5, Appli
14	37	82.2	9	6	US-11-007-740-18	Sequence 18, Appl
15	37	82.2	10	4	US-10-623-176-44	Sequence 44, Appl
16	37	82.2	12	4	US-10-623-176-65	Sequence 65, Appl
17	37	82.2	13	4	US-10-623-176-74	Sequence 74, Appl
18	37	82.2	13	4	US-10-791-217-14	Sequence 14, Appl
19	37	82.2	13	6	US-11-007-740-26	Sequence 26, Appl
20	36	80.0	9	4	US-10-623-176-1	Sequence 1, Appli
21	36	80.0	9	4	US-10-623-176-40	Sequence 40, Appl
22	36	80.0	9	4	US-10-791-217-1	Sequence 1, Appli
23	36	80.0	9	6	US-11-007-740-29	Sequence 29, Appl
24	36	80.0	10	4	US-10-623-176-6	Sequence 6, Appli
25	36	80.0	10	4	US-10-623-176-24	Sequence 24, Appl
26	36	80.0	13	4	US-10-623-176-54	Sequence 54, Appl
27	33	73.3	9	4	US-10-623-176-42	Sequence 42, Appl
28	33	73.3	9	4	US-10-623-176-46	Sequence 46, Appl
29	32	71.1	9	4	US-10-623-176-4	Sequence 4, Appli
30	32	71.1	14	4	US-10-623-176-50	Sequence 50, Appl
31	30	66.7	9	4	US-10-623-176-14	Sequence 14, Appl
32	30	66.7	9	4	US-10-791-217-4	Sequence 4, Appli
33	30	66.7	9	6	US-11-007-740-40	Sequence 40, Appl
34	29	64.4	9	4	US-10-623-176-48	Sequence 48, Appl
35	28.5	63.3	8	4	US-10-623-176-15	Sequence 15, Appl
36	28.5	63.3	8	6	US-11-007-740-38	Sequence 38, Appl
37	28	62.2	9	4	US-10-623-176-23	Sequence 23, Appl
38	28	62.2	9	4	US-10-623-176-38	Sequence 38, Appl
39	28	62.2	9	4	US-10-777-053-95	Sequence 95, Appl
40	28	62.2	9	4	US-10-837-217-95	Sequence 95, Appl
41	28	62.2	10	4	US-10-623-176-7	Sequence 7, Appli
42	28	62.2	13	4	US-10-623-176-64	Sequence 64, Appl
43	27	60.0	9	5	US-10-705-459-280	Sequence 280, App
44	27	60.0	10	4	US-10-623-176-8	Sequence 8, Appli
45	27	60.0	10	4	US-10-702-400-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
||||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H

```
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

  Query Match             100.0%;  Score 45;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 3
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
;  TITLE OF INVENTION:  of tumors
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

  Query Match             100.0%;  Score 45;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 4
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

  Query Match             100.0%;  Score 45;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 5
US-10-623-176-43
; Sequence 43, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(10)
US-10-623-176-43

  Query Match             100.0%;  Score 45;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 6
US-10-623-176-76
; Sequence 76, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
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```
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
;   OTHER INFORMATION: sequence derived from a presumed HA-1 homozygous
;   OTHER INFORMATION: positive individual
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(13)
US-10-623-176-76

  Query Match             100.0%;  Score 45;  DB 4;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          3 VLHDDLLEA 11


RESULT 7
US-10-791-217-16
; Sequence 16, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from HA-1+/+ phenotype
US-10-791-217-16

  Query Match             100.0%;  Score 45;  DB 4;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          3 VLHDDLLEA 11


RESULT 8
US-11-007-740-28
; Sequence 28, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-11-007-740-28

  Query Match             100.0%;  Score 45;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          3 VLHDDLLEA 11


RESULT 9
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-41

  Query Match             91.1%;  Score 41;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLE 8
              ||||||||
Db          2 VLHDDLLE 9


RESULT 10
US-10-623-176-45
; Sequence 45, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
```

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;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-45

  Query Match             91.1%;  Score 41;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDLLEA 9
              ||||||||
Db          1 LHDDLLEA 8


RESULT 11
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-10

  Query Match             82.2%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 12
US-10-623-176-47
; Sequence 47, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-47

  Query Match             82.2%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HDDLLEA 9
              |||||||
Db          1 HDDLLEA 7


RESULT 13
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5
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```
  Query Match             82.2%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 14
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

  Query Match             82.2%;  Score 37;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 15
US-10-623-176-44
; Sequence 44, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(10)
US-10-623-176-44

  Query Match             82.2%;  Score 37;  DB 4;  Length 10;
  Best Local Similarity   88.9%;  Pred. No. 4.4;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


Search completed: April  6, 2006, 17:28:45
Job time : 96.6667 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:24:07 ; Search time 12.6667 Seconds
(without alignments)
22.163 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 65691

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	7	US-11-010-748A-11	Sequence 11, Appl
2	37	82.2	9	7	US-11-010-748A-12	Sequence 12, Appl
3	26	57.8	6	7	US-11-129-143-163	Sequence 163, App
4	26	57.8	6	7	US-11-129-143-164	Sequence 164, App
5	26	57.8	6	7	US-11-129-143-165	Sequence 165, App
6	26	57.8	6	7	US-11-129-143-166	Sequence 166, App
7	25	55.6	6	7	US-11-129-143-161	Sequence 161, App
8	25	55.6	6	7	US-11-129-143-162	Sequence 162, App
9	24	53.3	8	7	US-11-004-399-1155	Sequence 1155, Ap
10	24	53.3	15	6	US-10-931-251A-13	Sequence 13, Appl
11	23	51.1	6	6	US-10-485-788A-353	Sequence 353, App
12	23	51.1	7	6	US-10-485-788A-354	Sequence 354, App
13	23	51.1	8	6	US-10-485-788A-355	Sequence 355, App
14	23	51.1	9	7	US-11-033-039-785	Sequence 785, App
15	23	51.1	9	7	US-11-033-039-809	Sequence 809, App
16	23	51.1	13	7	US-11-033-039-800	Sequence 800, App
17	23	51.1	13	7	US-11-033-039-821	Sequence 821, App
18	23	51.1	14	7	US-11-004-399-3188	Sequence 3188, Ap
19	23	51.1	14	7	US-11-004-399-3210	Sequence 3210, Ap
20	23	51.1	15	7	US-11-166-288-5	Sequence 5, Appli
21	23	51.1	15	7	US-11-166-288-11	Sequence 11, Appl
22	22	48.9	5	6	US-10-485-788A-352	Sequence 352, App
23	22	48.9	6	6	US-10-857-435A-443	Sequence 443, App
24	22	48.9	7	6	US-10-982-440-126	Sequence 126, App
25	22	48.9	8	7	US-11-045-024-444	Sequence 444, App
26	22	48.9	8	7	US-11-045-024-5467	Sequence 5467, Ap
27	22	48.9	8	7	US-11-045-024-7094	Sequence 7094, Ap
28	22	48.9	9	7	US-11-045-024-607	Sequence 607, App
29	22	48.9	9	7	US-11-045-024-3715	Sequence 3715, Ap
30	22	48.9	9	7	US-11-045-024-5511	Sequence 5511, Ap
31	22	48.9	9	7	US-11-045-024-12585	Sequence 12585, A
32	22	48.9	9	7	US-11-045-024-14029	Sequence 14029, A
33	22	48.9	10	6	US-10-989-767A-159	Sequence 159, App
34	22	48.9	10	6	US-10-989-767A-441	Sequence 441, App
35	22	48.9	10	6	US-10-989-767A-547	Sequence 547, App
36	22	48.9	10	7	US-11-045-024-61	Sequence 61, Appl
37	22	48.9	10	7	US-11-045-024-761	Sequence 761, App
38	22	48.9	10	7	US-11-045-024-762	Sequence 762, App
39	22	48.9	10	7	US-11-045-024-3822	Sequence 3822, Ap
40	22	48.9	10	7	US-11-045-024-3823	Sequence 3823, Ap
41	22	48.9	10	7	US-11-045-024-7092	Sequence 7092, Ap
42	22	48.9	10	7	US-11-045-024-7118	Sequence 7118, Ap
43	22	48.9	10	7	US-11-045-024-12588	Sequence 12588, A
44	22	48.9	11	7	US-11-045-024-906	Sequence 906, App
45	22	48.9	11	7	US-11-045-024-3923	Sequence 3923, Ap

ALIGNMENTS

RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T
; OTHER INFORMATION: ell epitopes
US-11-010-748A-11

Query Match 100.0%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

```
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
;  FILE REFERENCE: MER-136
;  CURRENT APPLICATION NUMBER: US/11/010,748A
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/EP03/06251
;  PRIOR FILING DATE: 2003-06-13
;  PRIOR APPLICATION NUMBER: EP02013423.5
;  PRIOR FILING DATE: 2002-06-13
;  NUMBER OF SEQ ID NOS: 926
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
;   OTHER INFORMATION: ell epitopes
US-11-010-748A-12

  Query Match             82.2%;  Score 37;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 3
US-11-129-143-163
; Sequence 163, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Bacillus stearothermophilus
US-11-129-143-163

  Query Match             57.8%;  Score 26;  DB 7;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              :||||
Db          1 IHDDL 5


RESULT 4
US-11-129-143-164
; Sequence 164, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Bacillus subtilis
US-11-129-143-164

  Query Match             57.8%;  Score 26;  DB 7;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              :||||
Db          1 IHDDL 5


RESULT 5
US-11-129-143-165
; Sequence 165, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-129-143-165

  Query Match             57.8%;  Score 26;  DB 7;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              :||||
Db          1 IHDDL 5


RESULT 6
US-11-129-143-166
; Sequence 166, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
;   LENGTH: 6
;   TYPE: PRT
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;   ORGANISM: Haemophilus influenzae
US-11-129-143-166

  Query Match            57.8%;  Score 26;  DB 7;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              :||||
Db          1 IHDDL 5


RESULT 7
US-11-129-143-161
; Sequence 161, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Bradyrhizobium japonicum
US-11-129-143-161

  Query Match            55.6%;  Score 25;  DB 7;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              :||||
Db          1 VHDDL 5


RESULT 8
US-11-129-143-162
; Sequence 162, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-162

  Query Match            55.6%;  Score 25;  DB 7;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDL 6
              :||||
Db          1 VHDDL 5


RESULT 9
US-11-004-399-1155
; Sequence 1155, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
;  APPLICANT: Chye, Mee Lee
;  APPLICANT:  Li, Hong Ye
;  APPLICANT:  Ramalingam, Sathiskumar
;  APPLICANT:  Poon, Leo Lit Man
;  APPLICANT:  Peiris, Joseph Sriyal Malik
;  TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
;  TITLE OF INVENTION:  Sequences and Methods of Use Thereof For Immunization Against SA
;  FILE REFERENCE: 2587/73166/RDK
;  CURRENT APPLICATION NUMBER: US/11/004,399
;  CURRENT FILING DATE:  2004-12-03
;  PRIOR APPLICATION NUMBER: US 60/527,637
;  PRIOR FILING DATE: 2003-12-03
;  NUMBER OF SEQ ID NOS: 4043
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1155
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: SARS-CoV Virus
US-11-004-399-1155

  Query Match            53.3%;  Score 24;  DB 7;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDD 5
              ||||
Db          3 LHDD 6


RESULT 10
US-10-931-251A-13
; Sequence 13, Application US/10931251A
; Publication No. US20060046277A1
; GENERAL INFORMATION:
;  APPLICANT: BELYAEV, ALEXANDER SERGEEVICH
;  APPLICANT:  KOLOKITHAS, ANGELO STEPHEN
;  APPLICANT:  MONELL, CRAIG ROBERT
;  TITLE OF INVENTION: PROTEIN KINASE AND PHOSPHATASE SUBSTRATES AND MULTIPLEX
;  TITLE OF INVENTION:  ASSAYS FOR IDENTIFYING THEIR ACTIVITIES
;  FILE REFERENCE: STG-106
;  CURRENT APPLICATION NUMBER: US/10/931,251A
;  CURRENT FILING DATE:  2004-09-01
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-931-251A-13

  Query Match            53.3%;  Score 24;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDD 5
              ||||
Db          2 LHDD 5


RESULT 11
US-10-485-788A-353
; Sequence 353, Application US/10485788A
```

```
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 353
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-353

  Query Match             51.1%;  Score 23;  DB 6;  Length 6;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::|||:
Db          1 LVHDDV 6


RESULT 12
US-10-485-788A-354
; Sequence 354, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 354
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-354

  Query Match             51.1%;  Score 23;  DB 6;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::|||:
Db          2 LVHDDV 7


RESULT 13
US-10-485-788A-355
; Sequence 355, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-355

  Query Match             51.1%;  Score 23;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::|||:
Db          3 LVHDDV 8


RESULT 14
US-11-033-039-785
; Sequence 785, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2017US01
;  CURRENT APPLICATION NUMBER: US/11/033,039
;  CURRENT FILING DATE:  2005-01-11
;  PRIOR APPLICATION NUMBER: 10/245,871
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 1452
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 785
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Zaire ebolavirus
US-11-033-039-785

  Query Match             51.1%;  Score 23;  DB 7;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              :||:  |:|
Db          1 LLHESTLKA 9


RESULT 15
US-11-033-039-809
; Sequence 809, Application US/11033039
; Publication No. US20060002947A1
```

; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 809
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Zaire ebolavirus
US-11-033-039-809

Query Match 51.1%; Score 23; DB 7; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.4e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 VLHDDLLEA 9
              :||:  |:|
Db          1 LLHESTLKA 9
```

Search completed: April 6, 2006, 17:29:30
Job time : 13.6667 secs

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:50:52 ; Search time 114 Seconds
(without alignments)
34.688 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	2	AAW99197	Aaw99197 Minor his
2	42	100.0	9	2	AAW97374	Aaw97374 HA-1 R-al
3	42	100.0	9	8	ADH40334	Adh40334 Human min
4	42	100.0	13	2	AAW99198	Aaw99198 DH cell K
5	42	100.0	13	2	AAW97414	Aaw97414 KIAA0223
6	37	88.1	9	2	AAW99196	Aaw99196 Minor his
7	37	88.1	9	2	AAW97375	Aaw97375 HA-1 H-al
8	37	88.1	9	8	ADH40333	Adh40333 Human min
9	37	88.1	13	2	AAW99199	Aaw99199 vR cell K
10	37	88.1	13	2	AAW97415	Aaw97415 KIAA0223
11	36	85.7	9	2	AAW99195	Aaw99195 Minor his
12	36	85.7	9	2	AAW97572	Aaw97572 T-cell ep
13	29	69.0	9	8	ADT73023	Adt73023 Human RSV
14	27	64.3	9	2	AAW47427	Aaw47427 Prenyl di
15	26	61.9	9	8	ADT73690	Adt73690 Human RSV
16	26	61.9	9	8	ADT72767	Adt72767 Human RSV
17	26	61.9	10	4	AAG94234	Aag94234 Human com
18	26	61.9	10	6	ABP71119	Abp71119 E10 prote
19	26	61.9	15	5	AAM47761	Aam47761 Ribosomal
20	25	59.5	9	5	AAU71428	Aau71428 Human MHC
21	25	59.5	9	8	ADT72766	Adt72766 Human RSV
22	25	59.5	9	8	ADT73689	Adt73689 Human RSV
23	25	59.5	10	2	AAW73901	Aaw73901 B. forsyt
24	25	59.5	10	8	ADQ26722	Adq26722 Topo V Hh
25	25	59.5	14	8	ADU38989	Adu38989 Mutant S1
26	25	59.5	15	5	ABB07889	Abb07889 Phosphoen
27	24	57.1	7	4	AAB81550	Aab81550 Zif268 zi
28	24	57.1	9	7	ADM18256	Adm18256 C trachom
29	24	57.1	9	7	ADM18218	Adm18218 Chlamydia
30	24	57.1	10	6	ABR04849	Abr04849 Human can
31	24	57.1	11	7	ADD23269	Add23269 Breast ca
32	24	57.1	12	2	AAW64577	Aaw64577 Human Fac
33	24	57.1	12	7	ADD23610	Add23610 Breast ca
34	24	57.1	13	5	ADG66269	Adg66269 Human pro
35	24	57.1	13	5	ADG66272	Adg66272 Human pro
36	24	57.1	13	5	ADG66271	Adg66271 Human pro
37	24	57.1	13	5	ADG66270	Adg66270 Human pro
38	24	57.1	13	7	ADD23767	Add23767 Breast ca
39	24	57.1	14	6	ABG74854	Abg74854 Human CHP
40	24	57.1	14	8	ADR73051	Adr73051 L plantar
41	24	57.1	15	6	ABR30509	Abr30509 Human can
42	24	57.1	15	6	ABR30940	Abr30940 Human can
43	24	57.1	15	6	ABR31271	Abr31271 Human can
44	24	57.1	15	6	ABR30473	Abr30473 Human can
45	24	57.1	15	6	ABR30612	Abr30612 Human can

ALIGNMENTS

RESULT 1
AAW99197
ID AAW99197 standard; peptide; 9 AA.
XX
AC AAW99197;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

```
  Query Match             100.0%;  Score 42;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 2
AAW97374
ID   AAW97374 standard; protein; 9 AA.
XX
AC   AAW97374;
XX
DT   13-MAY-1999  (first entry)
XX
DE   HA-1 R-allele sequence.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Claim 13; Fig 5; 59pp; English.
XX
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 R-allele. The specification describes methods for typing
CC   alleles (preferably the H and R alleles) of the minor histocompatibility
CC   antigen HA-1 in a sample, which comprise detecting polymorphic
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 42;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 3
ADH40334
ID   ADH40334 standard; peptide; 9 AA.
XX
AC   ADH40334;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 42;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 4
AAW99198
ID   AAW99198 standard; peptide; 13 AA.
XX
AC   AAW99198;
XX
DT   20-MAY-1999  (first entry)
XX
DE   DH cell KIAA0223 protein sequence.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
```

XX
OS Synthetic.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
DR N-PSDB; AAX19408.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 31; 47pp; English.
XX
CC The present invention describes a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases. The present sequence represents a KIAA0223 sequence given in
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 42; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 3 VLRDDLLEA 11

RESULT 5
AAW97414
ID AAW97414 standard; protein; 13 AA.
XX
AC AAW97414;
XX
DT 20-MAY-1999 (first entry)
XX
DE KIAA0223 polymorphism in HA-1 negative homozygous individuals.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
OS Homo sapiens.
XX
PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
DR N-PSDB; AAX16080.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Disclosure; Page 38; 57pp; English.
XX
CC The present sequence represents the KIAA0223 polymorphism in HA-1
CC negative homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or Graft-versus-Host
CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 42; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 3 VLRDDLLEA 11

RESULT 6
AAW99196
ID AAW99196 standard; peptide; 9 AA.
XX
AC AAW99196;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the

```
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             88.1%;  Score 37;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 7
AAW97375
ID   AAW97375 standard; protein; 9 AA.
XX
AC   AAW97375;
XX
DT   13-MAY-1999  (first entry)
XX
DE   HA-1 H-allele sequence.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Claim 18; Fig 5; 59pp; English.
XX
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 H-allele. The specification describes methods for typing
CC   alleles (preferably the H and R alleles) of the minor histocompatibility
CC   antigen HA-1 in a sample, which comprise detecting polymorphic
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             88.1%;  Score 37;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 8
ADH40333
ID   ADH40333 standard; peptide; 9 AA.
XX
AC   ADH40333;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             88.1%;  Score 37;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 9
AAW99199
ID   AAW99199 standard; peptide; 13 AA.
XX
AC   AAW99199;
XX
DT   20-MAY-1999  (first entry)
XX
```

DE vR cell KIAA0223 protein sequence.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Synthetic.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
DR N-PSDB; AAX19409.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 31; 47pp; English.
XX
CC The present invention describes a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases. The present sequence represents a KIAA0223 sequence given in
CC the present invention
XX
SQ Sequence 13 AA;

Query Match 88.1%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 3 VLHDDLLEA 11

RESULT 10
AAW97415
ID AAW97415 standard; protein; 13 AA.
XX
AC AAW97415;
XX
DT 20-MAY-1999 (first entry)
XX
DE KIAA0223 polymorphism in HA-1 positive homozygous individuals.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell; KIAA0223 polymorphism.
XX
OS Homo sapiens.
XX
PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
DR N-PSDB; AAX16081.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Disclosure; Page 38; 57pp; English.
XX
CC The present sequence represents the KIAA0223 polymorphism in HA-1
CC positive homozygous individuals. The specification describes an
CC immunogenic peptide constituting a T-cell epitope, obtainable from the
CC minor histocompatibility antigen HA-1. The peptide can be used in
CC vaccines or pharmaceutical formulations as medicines to induce tolerance
CC for transplants so as to prevent rejection and/or Graft-versus-Host
CC Disease, or to treat autoimmune diseases. Neoplastic haematopoietic cells
CC presenting the peptides, in an HLA class I context, can be eliminated
CC after specific recognition of the peptides. The peptides can also be used
CC to raise antibodies, T-cell receptor, B- and T-cells
XX
SQ Sequence 13 AA;

Query Match 88.1%; Score 37; DB 2; Length 13;
Best Local Similarity 88.9%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 3 VLHDDLLEA 11

RESULT 11
AAW99195
ID AAW99195 standard; peptide; 9 AA.
XX
AC AAW99195;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /label= His, Arg
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone

PT marrow and organ transplantation.
XX
PS Claim 1; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

Query Match 85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 1 VLXDDLLEA 9

RESULT 12
AAW97572
ID AAW97572 standard; peptide; 9 AA.
XX
AC AAW97572;
XX
DT 20-MAY-1999 (first entry)
XX
DE T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW neoplastic haematopoietic cell.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /note= "His or Arg"
XX
PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Claim 1; Page 39; 57pp; English.
XX
CC The present sequence represents an immunogenic peptide constituting a T-
CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC The peptide can be used in vaccines or pharmaceutical formulations as
CC medicines to induce tolerance for transplants so as to prevent rejection
CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC I context, can be eliminated after specific recognition of the peptides.
CC The peptides can also be used to raise antibodies, T-cell receptor, B-
CC and T-cells
XX
SQ Sequence 9 AA;

Query Match 85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 1 VLXDDLLEA 9

RESULT 13
ADT73023
ID ADT73023 standard; peptide; 9 AA.
XX
AC ADT73023;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 919.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 16; SEQ ID NO 919; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 69.0%; Score 29; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDLLEA 9
              :::||:| |
Db          1 IIKDDILSA 9
```

RESULT 14
AAW47427
ID AAW47427 standard; peptide; 9 AA.
XX
AC AAW47427;
XX
DT 05-JUN-1998 (first entry)
XX
DE Prenyl diphosphate synthetase preserved region VI sequence.
XX
KW Prenyl diphosphate synthetase; polyprenyl diphosphate; vitamin K;
KW ubiquinone; preserved region VI.
XX
OS Synthetic.
XX
PN EP812914-A2.
XX
PD 17-DEC-1997.
XX
PF 13-JUN-1997; 97EP-00109692.
XX
PR 14-JUN-1996; 96JP-00154441.
XX
PA (TOYT) TOYOTA JIDOSHA KK.
XX
PI Muramatsu M, Koike A, Ogura K, Koyama T, Shimizu N, Cho Y;
XX
DR WPI; 1998-034975/04.
XX
PT DNA encoding prenyl diphosphate synthetase subunit(s) - new Micrococcus
PT prenyl diphosphate synthetase subunit polypeptide(s), and methods for
PT preparing enzymes from subunit(s).
XX
PS Example 2; Page 26; 46pp; English.
XX
CC The present sequence from preserved region VI of prenyl diphosphate
CC synthetase (PDS), was used in the preparation of primers for the
CC amplification of PDS DNA. Substances synthesised by PDS, i.e. polyprenyl
CC diphosphates, are precursors of physiologically active substances, e.g.
CC vitamin K and ubiquinones
XX
SQ Sequence 9 AA;

Query Match 64.3%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 LRDDLLE 8
              :|||:|:
Db          3 IRDDILD 9
```

RESULT 15
ADT73690
ID ADT73690 standard; peptide; 9 AA.
XX
AC ADT73690;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 1586.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 16; SEQ ID NO 1586; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 61.9%; Score 26; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDLLEA 9
              :::||:| |
Db          1 IIKDDILLA 9
```

Search completed: April 6, 2006, 16:57:02
Job time : 114 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:57:26 ; Search time 19 Seconds
(without alignments)
45.576 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	50.0	15	2	A53594	calnexin - mouse (
2	19.5	46.4	15	2	S62675	collagen type I -
3	19	45.2	15	2	E56819	PS I complex subun
4	18	42.9	10	2	C26997	unspecific monooxy
5	18	42.9	12	2	S65730	hemoglobin, extrac
6	18	42.9	15	2	S71920	proteinase ECP 32
7	18	42.9	15	2	A26997	unspecific monooxy
8	17	40.5	11	2	PH0924	T-cell receptor be
9	17	40.5	11	2	S42449	ant1 protein - pha
10	17	40.5	12	2	S39762	cytochrome P450 UT
11	17	40.5	13	2	PS0443	potassium channel
12	17	40.5	14	2	S50900	chlorophyll a/b-bi
13	17	40.5	14	2	C39170	acyl-[acyl-carrier
14	17	40.5	15	2	S57584	T cell receptor V-
15	16	38.1	7	2	S68004	hucolin, 75K chain
16	16	38.1	8	2	PC4131	hypothetical prote
17	16	38.1	10	2	A61354	carnitine medium/l
18	16	38.1	10	2	S13224	virG protein - Agr
19	16	38.1	12	2	PH1605	Ig H chain V-D-J r
20	16	38.1	13	2	S14316	photosystem I 9K c
21	16	38.1	13	4	I70075	glycophorin B (mis
22	16	38.1	14	2	S29789	hypothetical prote
23	16	38.1	15	2	B32800	hypothetical prote
24	16	38.1	15	2	PH1378	T antigen variant
25	16	38.1	15	2	PH1377	T antigen variant
26	15	35.7	7	2	A59489	protein kinase C i
27	15	35.7	10	2	F44644	neurotoxin-associa
28	15	35.7	11	2	PT0249	Ig heavy chain CRD
29	15	35.7	11	4	S41909	hypothetical prote
30	15	35.7	13	2	S12388	argA protein - Sal
31	15	35.7	13	2	S65612	tubulin alpha-chai
32	15	35.7	13	2	PC1008	40K extracellular
33	15	35.7	13	2	G44644	neurotoxin-associa
34	15	35.7	13	2	S00316	photosystem I 13K
35	15	35.7	14	2	S57569	T cell receptor V-
36	15	35.7	14	2	A61306	ribonuclease M (EC
37	15	35.7	15	2	PQ0750	self-incompatibili
38	15	35.7	15	2	PN0629	integration host f
39	15	35.7	15	2	C43334	orf3 3' to aadR -
40	15	35.7	15	2	D54226	light-harvesting p
41	14.5	34.5	15	2	D60977	14K protein - Cali
42	14	33.3	7	2	S20446	elastase - Pseudom
43	14	33.3	9	2	A60427	macrophage cytotox
44	14	33.3	10	2	E86128	hypothetical prote
45	14	33.3	11	2	C53652	rhlR protein - Pse

ALIGNMENTS

RESULT 1
A53594
calnexin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A53594
R;Lenter, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A;Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin pr
A;Reference number: A53594; MUID:94216347; PMID:8163531
A;Accession: A53594
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <LEN>
A;Cross-references: UNIPROT:Q7M063; UNIPARC:UPI000017C62E
C;Keywords: endoplasmic reticulum; molecular chaperone

Query Match 50.0%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDL 6
              :: |||
Db         10 IIEDDL 15
```

RESULT 2
S62675
collagen type I - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62675
R;Mizuno, M.; Kitafima, T.; Tomita, M.; Kuboki, Y.
Biochim. Biophys. Acta 1310, 97-102, 1996
A;Title: The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of type I col
A;Reference number: S62675; MUID:97386332; PMID:9244181
A;Accession: S62675
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <MIZ>
A;Cross-references: UNIPROT:Q7M062; UNIPARC:UPI000017C63D

Query Match 46.4%; Score 19.5; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 VLRD-DLLE 8
              | || |:||
Db          7 VQRDRDILE 15
```

RESULT 3

```
E56819
PS I complex subunit 8 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: E56819
R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A;Reference number: A56819; MUID:91355209; PMID:1883835
A;Accession: E56819
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <IWA>
A;Cross-references: UNIPROT:P42052; UNIPARC:UPI0000132593
A;Note: sequence extracted from NCBI backbone (NCBIP:58606)

  Query Match             45.2%;  Score 19;  DB 2;  Length 15;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDD 5
              |::||
Db         10 VIQDD 14


RESULT 4
C26997
unspecific monooxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic - ra
N;Alternate names: cytochrome P450
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: C26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A;Reference number: A26997; MUID:88000604; PMID:3651420
A;Accession: C26997
A;Molecule type: protein
A;Residues: 1-10 <GRA>
A;Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA8
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

  Query Match             42.9%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              ||| |
Db          2 DLLSA 6


RESULT 5
S65730
hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65730
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
A;Reference number: S65721; MUID:96176855; PMID:8597573
A;Accession: S65730
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FUS>
A;Cross-references: UNIPARC:UPI000017BD88

  Query Match             42.9%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              || |::
Db          6 RDHLIQ 11


RESULT 6
S71920
proteinase ECP 32 (EC 3.4.24.-) - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71920
R;Matveyev, V.V.; Usmanova, A.M.; Morozova, A.V.; Collins, J.H.; Khaitlina, S.Y.
Biochim. Biophys. Acta 1296, 55-62, 1996
A;Title: Purification and characterization of the proteinase ECP 32 from Escherichia col
A;Reference number: S71920; MUID:96350420; PMID:8765229
A;Accession: S71920
A;Molecule type: protein
A;Residues: 1-15 <MAT>
A;Cross-references: UNIPROT:Q9R4D6; UNIPARC:UPI00000B73DB
A;Experimental source: strain A2
C;Keywords: hydrolase; metalloproteinase

  Query Match             42.9%;  Score 18;  DB 2;  Length 15;
  Best Local Similarity   57.1%;  Pred. No. 2.4e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLRDDLL 7
              |:||  |
Db          9 VIRDIFL 15


RESULT 7
A26997
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment)
N;Alternate names: cytochrome P450b
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: A26997
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A;Reference number: A26997; MUID:88000604; PMID:3651420
A;Accession: A26997
A;Molecule type: protein
A;Residues: 1-15 <GRA>
A;Cross-references: UNIPROT:Q06884; UNIPARC:UPI0000174DA7
C;Superfamily: cytochrome P450 homology
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

  Query Match             42.9%;  Score 18;  DB 2;  Length 15;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              ||| |
Db          2 DLLSA 6


RESULT 8
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Cross-references: UNIPARC:UPI000017C9F3
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor
```

Query Match 40.5%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 DLLE 8
              ||:|
Db          7 DLME 10
```

RESULT 9
S42449
antl protein - phage P7
C;Species: phage P7
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S42449
R;Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A;Reference number: S42448; MUID:90335968; PMID:1696181
A;Accession: S42449
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <CIT>
A;Cross-references: UNIPROT:Q38415; UNIPARC:UPI000009B041; EMBL:M35139; NID:g215705; PID

Query Match 40.5%; Score 17; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDL 6
              | |:|:
Db          6 VTRNDI 11
```

RESULT 10
S39762
cytochrome P450 UT-7b - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S39762
R;Ohishi, N.; Imaoka, S.; Suzuki, T.; Funae, Y.
Biochim. Biophys. Acta 1158, 227-236, 1993
A;Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
A;Reference number: S39761; MUID:94072607; PMID:8251521
A;Accession: S39762
A;Molecule type: protein
A;Residues: 1-12 <OHI>
A;Cross-references: UNIPARC:UPI000017C8F7

Query Match 40.5%; Score 17; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDL 6
              :: |||
Db          3 LIGDDL 8
```

RESULT 11
PS0443
potassium channel protein Slo G3 - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C;Accession: PS0443
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A;Reference number: JH0697; MUID:92360298; PMID:1497890
A;Accession: PS0443
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-13 <ADE>
A;Cross-references: UNIPARC:UPI000017BEBA
C;Comment: This potassium channel is activated by calcium.
C;Genetics:
A;Gene: FlyBase:slo
A;Cross-references: FlyBase:FBgn0003429
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 40.5%; Score 17; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 DDLL 7
              |||:
Db         10 DDLV 13
```

RESULT 12
S50900
chlorophyll a/b-binding protein Lhcb5 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIc protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50900
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclol
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50900
A;Molecule type: protein
A;Residues: 1-14 <WAL>
A;Cross-references: UNIPARC:UPI0000178182
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosys

Query Match 40.5%; Score 17; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 RDD 5
              |||
Db         10 RDD 12
```

RESULT 13
C39170
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - avocado (fragments)
C;Species: Persea americana (avocado)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002
C;Accession: C39170
R;Shanklin, J.; Somerville, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A;Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally unr
A;Reference number: A39170; MUID:91172837; PMID:2006187
A;Accession: C39170
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <SHA>
A;Cross-references: UNIPARC:UPI000017CD5B
C;Keywords: oxidoreductase

Query Match 40.5%; Score 17; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 DLLE 8
              |:||
Db         11 DILE 14
```

RESULT 14
S57584
T cell receptor V-D-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)

```
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57584
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A;Reference number: S57494
A;Accession: S57584
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <BUR>
A;Cross-references: UNIPARC:UPI0000116747; EMBL:Z49956; NID:g887466; PIDN:CAA90227.1; PI
C;Keywords: T-cell receptor

  Query Match             40.5%;  Score 17;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDD 5
              |||
Db          8 RDD 10


RESULT 15
S68004
hucolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>
A;Cross-references: UNIPARC:UPI000017C164

  Query Match             38.1%;  Score 16;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDL 6
              |||
Db          4 DDL 6


Search completed: April  6, 2006, 17:03:59
Job time : 20 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:51:26 ; Search time 116.333 Seconds
(without alignments)
54.582 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	59.5	11	2	Q47600_ECOLI	Q47600 escherichia
2	21	50.0	10	2	Q718N9_9PARA	Q718n9 newcastle d
3	21	50.0	11	1	UF05_MOUSE	P38643 mus musculu
4	21	50.0	11	2	Q718K6_9PARA	Q718k6 newcastle d
5	21	50.0	15	1	UC27_MAIZE	P80633 zea mays (m
6	21	50.0	15	2	Q7M063_MOUSE	Q7m063 mus musculu
7	20	47.6	13	2	P82560_STRPY	P82560 streptococc
8	19.5	46.4	15	2	Q7M062_MOUSE	Q7m062 mus musculu
9	19	45.2	10	2	Q9UWM5_SULSO	Q9uwm5 sulfolobus
10	19	45.2	11	2	Q9UNL8_HUMAN	Q9unl8 homo sapien
11	19	45.2	11	2	Q47602_ECOLI	Q47602 escherichia
12	19	45.2	14	2	Q9ZB42_STRPY	Q9zb42 streptococc
13	19	45.2	15	1	PSAO_CUCSA	P42052 cucumis sat
14	19	45.2	15	2	Q9UC60_HUMAN	Q9uc60 homo sapien
15	19	45.2	15	2	Q9UCZ7_HUMAN	Q9ucz7 homo sapien
16	19	45.2	15	2	Q9TRN6_PIG	Q9trn6 sus scrofa
17	19	45.2	15	2	Q9R5D6_CHRVI	Q9r5d6 chromatium
18	18	42.9	8	2	Q7XB03_MAIZE	Q7xb03 zea mays (m
19	18	42.9	9	2	Q7X8P7_MAIZE	Q7x8p7 zea mays (m
20	18	42.9	12	1	XYLA_STRVN	P14405 streptomyce
21	18	42.9	12	2	Q9T2U3_BOVIN	Q9t2u3 bos taurus
22	18	42.9	12	2	Q9TQY4_BOVIN	Q9tqy4 bos taurus
23	18	42.9	12	2	Q5MK49_9CLOS	Q5mk49 citrus tris
24	18	42.9	12	2	Q5MK52_9CLOS	Q5mk52 citrus tris
25	18	42.9	12	2	Q5MK66_9CLOS	Q5mk66 citrus tris
26	18	42.9	12	2	Q5MK81_9CLOS	Q5mk81 citrus tris
27	18	42.9	13	1	UN02_PINPS	P81667 pinus pinas
28	18	42.9	13	2	Q7XB02_MAIZE	Q7xb02 zea mays (m
29	18	42.9	13	2	Q7TE19_9CLOS	Q7te19 citrus tris
30	18	42.9	13	2	Q7TE20_9CLOS	Q7te20 citrus tris
31	18	42.9	13	2	Q7TE23_9CLOS	Q7te23 citrus tris
32	18	42.9	13	2	Q7TE26_9CLOS	Q7te26 citrus tris
33	18	42.9	13	2	Q7TE30_9CLOS	Q7te30 citrus tris
34	18	42.9	13	2	Q957T7_9PERC	Q957t7 trichopsis
35	18	42.9	14	2	Q7X8P6_MAIZE	Q7x8p6 zea mays (m
36	18	42.9	14	2	Q52840_RHILO	Q52840 rhizobium l
37	18	42.9	15	2	Q7XB01_MAIZE	Q7xb01 zea mays (m
38	18	42.9	15	2	Q9R4D6_ECOLI	Q9r4d6 escherichia
39	17	40.5	10	2	Q5S732_9FUNG	Q5s732 glomus cale
40	17	40.5	10	2	Q5S733_9FUNG	Q5s733 glomus geos
41	17	40.5	10	2	Q9TQV4_HORSE	Q9tqv4 e equus cab
42	17	40.5	11	2	Q5IKF0_HUMAN	Q5ikf0 homo sapien
43	17	40.5	11	2	Q38415_BPP7	Q38415 bacteriopha
44	17	40.5	12	2	Q9XS31_PIG	Q9xs31 sus scrofa
45	17	40.5	12	2	Q7GCS7_ORYSA	Q7gcs7 oryza sativ

ALIGNMENTS

RESULT 1
Q47600_ECOLI
ID Q47600_ECOLI PRELIMINARY; PRT; 11 AA.
AC Q47600;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN Name=REase;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63619; AAA24556.1; -; Genomic_DNA.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;

Query Match 59.5%; Score 25; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 LRDDLLEA 9
              || ||: |
Db          3 LRSDLINA 10
```

RESULT 2
Q718N9_9PARA
ID Q718N9_9PARA PRELIMINARY; PRT; 10 AA.
AC Q718N9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemagglutinin-neuraminidase (Fragment).
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gould A.R., Hansson E., Selleck K., Kattenbelt J.A., Mackenzie M.,
RA Della-Porta A.J.;
RT "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
RT motifs as markers for viral lineage.";
RL Avian Pathol. 32:361-373(2003).
DR EMBL; AF542884; AAQ11609.1; -; Genomic_DNA.
FT NON_TER 1 1

```
SQ   SEQUENCE   10 AA;  1100 MW;  711806AAA337205B CRC64;

  Query Match             50.0%;  Score 21;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 3.1e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDD 5
              :|:||
Db          4 ILKDD 8


RESULT 3
UF05_MOUSE
ID   UF05_MOUSE     STANDARD;      PRT;    11 AA.
AC   P38643;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Unknown protein from 2D-PAGE of fibroblasts (P48) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins using
RT   preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 5.5, its MW is: 48 kDa.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   Direct protein sequencing.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1330 MW;  E54835E5CAAABAFA CRC64;

  Query Match             50.0%;  Score 21;  DB 1;  Length 11;
  Best Local Similarity   37.5%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              :  ||::|
Db          3 IXXDDVIE 10


RESULT 4
Q718K6_9PARA
ID   Q718K6_9PARA PRELIMINARY;      PRT;    11 AA.
AC   Q718K6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hemagglutinin-neuraminidase (Fragment).
OS   Newcastle disease virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX   NCBI_TaxID=11176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gould A.R., Hansson E., Selleck K., Kattenbelt J.A., Mackenzie M.,
RA   Della-Porta A.J.;
RT   "Newcastle disease virus fusion and hemagglutinin-neuraminidase gene
RT   motifs as markers for viral lineage.";
RL   Avian Pathol. 32:361-373(2003).
DR   EMBL; AF542917; AAQ11642.1; -; Genomic_DNA.
FT   NON_TER      1      1
SQ   SEQUENCE   11 AA;  1313 MW;  710428D6A337205B CRC64;

  Query Match             50.0%;  Score 21;  DB 2;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 3.4e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDD 5
              :|:||
Db          5 ILKDD 9


RESULT 5
UC27_MAIZE
ID   UC27_MAIZE     STANDARD;      PRT;    15 AA.
AC   P80633;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 688)
DE   (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Coleoptile;
RA   Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA   Pernollet J.-C., Zivy M., de Vienne D.;
RT   "The maize two dimensional gel protein database: towards an integrated
RT   genome analysis program.";
RL   Theor. Appl. Genet. 93:997-1005(1996).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 6.4, its MW is: 48.4 kDa.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   Maize-2DPAGE; P80633; COLEOPTILE.
DR   Gramene; P80633; -.
DR   MaizeDB; 123958; -.
KW   Direct protein sequencing.
FT   NON_TER      1      1
FT   NON_TER     15     15
SQ   SEQUENCE   15 AA;  1853 MW;  CA0E12A5DAED8DC7 CRC64;

  Query Match             50.0%;  Score 21;  DB 1;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 4.8e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LRDDLLEA 9
              ||| : :|
Db          5 LRDQVYDA 12


RESULT 6
Q7M063_MOUSE
ID   Q7M063_MOUSE PRELIMINARY;      PRT;    15 AA.
AC   Q7M063;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Calnexin (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
```

```
OX   NCBI_TaxID=10090;.
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=94216347; PubMed=8163531;
RA   Lenter M., Vestweber D.;
RT   "The integrin chains beta-1 and alpha-6 associate with the chaperone
RT   calnexin prior to integrin assembly.";
RL   J. Biol. Chem. 269:12263-12268(1994).
DR   PIR; A53594; A53594.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1693 MW;  C62AAAA42F9F5F35 CRC64;

  Query Match             50.0%;  Score 21;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 4.8e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDL 6
              :: |||
Db         10 IIEDDL 15


RESULT 7
P82560_STRPY
ID   P82560_STRPY  PRELIMINARY;      PRT;    13 AA.
AC   P82560;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Unknown protein from 2D-page (Fragment).
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC   STRAIN=JRS4;
RA   Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA   VanBogelen R.A.;
RT   "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT   proteins.";
RL   Submitted (MAY-2000) to Swiss-Prot.
CC   -!- MASS SPECTROMETRY: MW=30142.85; METHOD=Electrospray.
FT   NON_TER       1      1
FT   NON_TER      13     13
SQ   SEQUENCE   13 AA;  1464 MW;  CFE7DB129CE0C6D9 CRC64;

  Query Match             47.6%;  Score 20;  DB 2;  Length 13;
  Best Local Similarity   37.5%;  Pred. No. 6.5e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LRDDLLEA 9
              : ||: :|
Db          1 ITDDVFQA 8


RESULT 8
Q7M062_MOUSE
ID   Q7M062_MOUSE PRELIMINARY;      PRT;    15 AA.
AC   Q7M062;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Collagen type I (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=97386332; PubMed=9244181; DOI=10.1016/0167-4889(95)00151-4;
RA   Mizuno M., Kitafima T., Tomita M., Kuboki Y.;
RT   "The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of
RT   type I collagen, which promoted cell-attachment of osteoblasts.";
RL   Biochim. Biophys. Acta 1310:97-102(1996).
DR   PIR; S62675; S62675.
FT   NON_TER       1      1
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1729 MW;  DCDBF2FCE50EE542 CRC64;

  Query Match             46.4%;  Score 19.5;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 9.5e+03;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 VLRD-DLLE 8
              | || |:||
Db          7 VQRDRDILE 15


RESULT 9
Q9UWM5_SULSO
ID   Q9UWM5_SULSO PRELIMINARY;      PRT;    10 AA.
AC   Q9UWM5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Ribosomal protein L4 (Fragment).
OS   Sulfolobus solfataricus.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=2287;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=92042057; PubMed=1939187;
RA   Casiano C., Traut R.R.;
RT   "Protein topography of Sulfolobus solfataricus ribosomes by cross-
RT   linking with 2-iminothiolane. Sso L12e, Sso L10e, and Sso L11e are
RT   neighbors.";
RL   J. Biol. Chem. 266:21578-21583(1991).
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1134 MW;  C0336E35BAA33AAD CRC64;

  Query Match             45.2%;  Score 19;  DB 2;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 7.7e+03;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              :| |:|
Db          5 KDSLIE 10


RESULT 10
Q9UNL8_HUMAN
ID   Q9UNL8_HUMAN PRELIMINARY;      PRT;    11 AA.
AC   Q9UNL8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   APC2 protein (Fragment).
GN   Name=APC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,
RA   Meredith D.M.;
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF110338; AAD29275.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1326 MW;  75881D7BB441EAB4 CRC64;
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  Query Match             45.2%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRD 4
              ||||
Db          2 VLRD 5


RESULT 11
Q47602_ECOLI
ID   Q47602_ECOLI PRELIMINARY;      PRT;    11 AA.
AC   Q47602;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   REase protein (Fragment).
GN   Name=REase;
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91139577; PubMed=1995588;
RA   Tao T., Bourne J.C., Blumenthal R.M.;
RT   "A family of regulatory genes associated with type II restriction-
RT   modification systems.";
RL   J. Bacteriol. 173:1367-1375(1991).
DR   EMBL; M63620; AAA24558.1; -; Genomic_DNA.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1412 MW;  80ABB190C736DAAA CRC64;

  Query Match             45.2%;  Score 19;  DB 2;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 8.5e+03;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLL 7
              ||| |
Db          3 RDDQL 7


RESULT 12
Q9ZB42_STRPY
ID   Q9ZB42_STRPY PRELIMINARY;      PRT;    14 AA.
AC   Q9ZB42;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   SsbA (Fragment).
GN   Name=ssbA;
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CS101;
RA   Podbielski A., Woischnik M., Leonard B.A.B., Schmidt K.H.;
RT   "Characterization of nra, a global negative regulator gene in group A
RT   streptococci.";
RL   Mol. Microbiol. 31:0-0(1999).
DR   EMBL; U49397; AAC97153.1; -; Genomic_DNA.
FT   NON_TER      1      1
SQ   SEQUENCE   14 AA;  1618 MW;  47074F277A834F17 CRC64;

  Query Match             45.2%;  Score 19;  DB 2;  Length 14;
  Best Local Similarity   57.1%;  Pred. No. 1.1e+04;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLRDDLL 7
              || :| |
Db          6 VLEEDTL 12


RESULT 13
PSAO_CUCSA
ID   PSAO_CUCSA     STANDARD;      PRT;    15 AA.
AC   P42052;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Photosystem 1 reaction centre subunit 8 (Photosystem I 17.5 kDa
DE   protein) (Fragment).
GN   Name=PSAM;
OS   Cucumis sativus (Cucumber).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX   NCBI_TaxID=3659;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   TISSUE=Cotyledon;
RX   MEDLINE=91355209; PubMed=1883835;
RA   Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT   "Characterization of genes that encode subunits of cucumber PS I
RT   complex by N-terminal sequencing.";
RL   Biochim. Biophys. Acta 1059:141-148(1991).
CC   -!- FUNCTION: Essential for the activity of NADP photoreduction.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; E56819; E56819.
KW   Chloroplast; Direct protein sequencing; Membrane; Photosynthesis;
KW   Photosystem I; Thylakoid.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1715 MW;  CA0BF5DAD403D9F4 CRC64;

  Query Match             45.2%;  Score 19;  DB 1;  Length 15;
  Best Local Similarity   60.0%;  Pred. No. 1.2e+04;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDD 5
              |::||
Db         10 VIQDD 14


RESULT 14
Q9UC60_HUMAN
ID   Q9UC60_HUMAN  PRELIMINARY;      PRT;    15 AA.
AC   Q9UC60;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   N-acetylmuramyl-L-alanine amidase (EC 3.5.1.28) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=95392215; PubMed=7663175; DOI=10.1006/prep.1995.1049;
RA   De Pauw P., Neyt C., Vanderwinkel E., Wattiez R., Falmagne P.;
RT   "Characterization of human serum N-acetylmuramyl-L-alanine amidase
RT   purified by affinity chromatography.";
RL   Protein Expr. Purif. 6:371-378(1995).
DR   GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; TAS.
DR   GO; GO:0001519; P:peptide amidation; NAS.
SQ   SEQUENCE   15 AA;  1600 MW;  9016B00FFF9E780A CRC64;

  Query Match             45.2%;  Score 19;  DB 2;  Length 15;
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Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 VLRDDLLEA 9
              :| | :::|
Db          4 LLMDSVIQA 12
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RESULT 15
Q9UCZ7_HUMAN
ID Q9UCZ7_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q9UCZ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE BCL2-interactive cell death susceptibility regulator (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96071131; PubMed=7475270;
RA Meijerink J.P., Smetsers T.F., Sloetjes A.W., Linders E.H.,
RA Mensink E.J.;
RT "Bax mutations in cell lines derived from hematological
RT malignancies.";
RL Leukemia 9:1828-1832(1995).
SQ SEQUENCE 15 AA; 1860 MW; 4F9238D6FE9743DB CRC64;

Query Match 45.2%; Score 19; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 LRDDL 6
              :||:|
Db          4 IRDEL 8
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Job time : 116.333 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:03:16 ; Search time 27.6667 Seconds
(without alignments)
26.894 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	2	US-09-269-250E-18	Sequence 18, Appl
2	42	100.0	9	2	US-09-489-760-5	Sequence 5, Appli
3	42	100.0	13	2	US-09-269-250E-26	Sequence 26, Appl
4	42	100.0	13	2	US-09-489-760-14	Sequence 14, Appl
5	37	88.1	9	2	US-09-269-250E-20	Sequence 20, Appl
6	37	88.1	9	2	US-09-489-760-2	Sequence 2, Appli
7	37	88.1	13	2	US-09-269-250E-28	Sequence 28, Appl
8	37	88.1	13	2	US-09-489-760-16	Sequence 16, Appl
9	36	85.7	9	2	US-09-269-250E-29	Sequence 29, Appl
10	36	85.7	9	2	US-09-489-760-1	Sequence 1, Appli
11	27	64.3	9	2	US-09-217-609A-11	Sequence 11, Appl
12	27	64.3	9	2	US-08-873-235B-11	Sequence 11, Appl
13	23	54.8	8	2	US-09-269-250E-38	Sequence 38, Appl
14	23	54.8	11	2	US-09-972-115A-64	Sequence 64, Appl
15	23	54.8	14	1	US-08-962-284-8	Sequence 8, Appli
16	23	54.8	14	2	US-09-205-258-839	Sequence 839, App
17	23	54.8	14	2	US-10-004-860-839	Sequence 839, App
18	22	52.4	7	2	US-08-556-419-14	Sequence 14, Appl
19	22	52.4	9	2	US-09-489-760-4	Sequence 4, Appli
20	22	52.4	12	1	US-08-685-357B-12	Sequence 12, Appl
21	22	52.4	12	2	US-09-569-037-1	Sequence 1, Appli
22	22	52.4	14	2	US-09-747-287A-102	Sequence 102, App
23	22	52.4	15	2	US-08-940-095-104	Sequence 104, App
24	22	52.4	15	2	US-08-940-093-104	Sequence 104, App
25	22	52.4	15	2	US-08-940-096-104	Sequence 104, App
26	22	52.4	15	2	US-09-465-719-104	Sequence 104, App
27	22	52.4	15	2	US-09-453-605-104	Sequence 104, App
28	22	52.4	15	2	US-09-453-838-104	Sequence 104, App
29	22	52.4	15	2	US-09-561-490E-4	Sequence 4, Appli
30	22	52.4	15	2	US-08-940-136-104	Sequence 104, App
31	22	52.4	15	2	US-09-453-841-104	Sequence 104, App
32	22	52.4	15	2	US-09-453-833-104	Sequence 104, App
33	22	52.4	15	2	US-09-453-826-104	Sequence 104, App
34	22	52.4	15	2	US-09-050-739-79	Sequence 79, Appl
35	22	52.4	15	2	US-09-453-840-104	Sequence 104, App
36	22	52.4	15	2	US-09-865-989-104	Sequence 104, App
37	22	52.4	15	2	US-09-453-834-104	Sequence 104, App
38	22	52.4	15	2	US-10-283-599-104	Sequence 104, App
39	22	52.4	15	2	US-09-465-718-104	Sequence 104, App
40	21	50.0	6	1	US-08-459-568-20	Sequence 20, Appl
41	21	50.0	6	1	US-08-399-411-20	Sequence 20, Appl
42	21	50.0	6	2	US-08-516-859A-20	Sequence 20, Appl
43	21	50.0	6	2	US-09-586-472-20	Sequence 20, Appl
44	21	50.0	6	2	US-09-528-706-20	Sequence 20, Appl
45	21	50.0	7	2	US-10-122-675-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA

US-09-489-760-5

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 1 VLRDDLLEA 9

RESULT 3
US-09-269-250E-26
; Sequence 26, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-26

Query Match 100.0%; Score 42; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 3 VLRDDLLEA 11

RESULT 4
US-09-489-760-14
; Sequence 14, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:HA-1-/-
US-09-489-760-14

Query Match 100.0%; Score 42; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 3 VLRDDLLEA 11

RESULT 5
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 6
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
US-09-489-760-2

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 7
US-09-269-250E-28
; Sequence 28, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-09-269-250E-28

  Query Match             88.1%;  Score 37;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 0.29;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          3 VLHDDLLEA 11


RESULT 8
US-09-489-760-16
; Sequence 16, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism:HA-1+/+
US-09-489-760-16

  Query Match             88.1%;  Score 37;  DB 2;  Length 13;
  Best Local Similarity   88.9%;  Pred. No. 0.29;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          3 VLHDDLLEA 11


RESULT 9
US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

  Query Match             85.7%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 10
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
;   OTHER INFORMATION: RESIDUE
US-09-489-760-1

  Query Match             85.7%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 11
US-09-217-609A-11
; Sequence 11, Application US/09217609A
; Patent No. 6071733
;  GENERAL INFORMATION:
;    APPLICANT:  MURAMATSU, Masayoshi
;    APPLICANT:  KOIKE, Ayumi
;    APPLICANT:  OGURA, Kyozo
;    APPLICANT:  KOYAMA, Tanetoshi
;    APPLICANT:  SHIMIZU, Naoto
;    APPLICANT:  CHO, Yenwin
;    TITLE OF INVENTION:  Prenyl Diphosphate Synthetase Genes
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, NW - Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/09/217,609A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/873,235
;      FILING DATE:  11-Jun-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TOFFENETTI, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  10235/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-217-609A-11

  Query Match             64.3%;  Score 27;  DB 2;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLLE 8
              :|||:|:
Db          3 IRDDILD 9


RESULT 12
US-08-873-235B-11
; Sequence 11, Application US/08873235B
; Patent No. 6174715
;  GENERAL INFORMATION:
;    APPLICANT:  MURAMATSU, Masayoshi
;    APPLICANT:  KOIKE, Ayumi
;    APPLICANT:  OGURA, Kyozo
;    APPLICANT:  KOYAMA, Tanetoshi
;    APPLICANT:  SHIMIZU, Naoto
;    APPLICANT:  CHO, Yenwin
;    TITLE OF INVENTION:  Prenyl Diphosphate Synthetase Genes
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, NW - Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/873,235B
;      FILING DATE:  11-Jun-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 154441/1996
;      FILING DATE:  14-Jun-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TOFFENETTI, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  10235/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-873-235B-11

  Query Match             64.3%;  Score 27;  DB 2;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLLE 8
              :|||:|:
Db          3 IRDDILD 9


RESULT 13
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-269-250E-38

  Query Match             54.8%;  Score 23;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              |||||
Db          4 DLLEA 8


RESULT 14
US-09-972-115A-64
; Sequence 64, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
;  APPLICANT: Geron Corporation
;  APPLICANT:  Gregg, Morin B.
;  APPLICANT:  Walter, Funk D.
;  APPLICANT:  Mieczyslaw, Piatyszek A.
;  TITLE OF INVENTION: A Second Mammalian Telomerase
;  FILE REFERENCE: 080/003C
;  CURRENT APPLICATION NUMBER: US/09/972,115A
;  CURRENT FILING DATE:  2001-10-05
;  PRIOR APPLICATION NUMBER: US 60/128,577
;  PRIOR FILING DATE: 2000-04-10
;  PRIOR APPLICATION NUMBER: US 60/129,123
;  PRIOR FILING DATE: 1999-04-13
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-972-115A-64

  Query Match             54.8%;  Score 23;  DB 2;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              :|:|||
Db          5 KDELLE 10
```

```
RESULT 15
US-08-962-284-8
; Sequence 8, Application US/08962284
; Patent No. 5985608
;  GENERAL INFORMATION:
;    APPLICANT:  Luna, Elizabeth J.
;    APPLICANT:  Pestonjamasp, Kersi N.
;    APPLICANT:  Pope, Robert K.
;    APPLICANT:  Wulfkuhle, Julia D.
;    TITLE OF INVENTION:  ACTIN-BINDING POLYPEPTIDES
;    TITLE OF INVENTION:  AND NUCLEIC ACIDS ENCODING THE SAME
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/962,284
;      FILING DATE:  31-OCT-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, Peter J.
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  07917/058001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-962-284-8

  Query Match             54.8%;  Score 23;  DB 1;  Length 14;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              |:|||:
Db          6 REDLLQ 11


Search completed: April  6, 2006, 17:05:28
Job time : 28.6667 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 17:22:22 ; Search time 96.6667 Seconds
(without alignments)
38.901 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	4	US-10-623-176-10	Sequence 10, Appl
2	42	100.0	9	4	US-10-791-217-5	Sequence 5, Appli
3	42	100.0	9	6	US-11-007-740-18	Sequence 18, Appl
4	42	100.0	10	4	US-10-623-176-44	Sequence 44, Appl
5	42	100.0	12	4	US-10-623-176-65	Sequence 65, Appl
6	42	100.0	13	4	US-10-623-176-74	Sequence 74, Appl
7	42	100.0	13	4	US-10-791-217-14	Sequence 14, Appl
8	42	100.0	13	6	US-11-007-740-26	Sequence 26, Appl
9	38	90.5	9	4	US-10-623-176-42	Sequence 42, Appl
10	38	90.5	9	4	US-10-623-176-46	Sequence 46, Appl
11	37	88.1	9	4	US-10-623-176-2	Sequence 2, Appli
12	37	88.1	9	4	US-10-791-217-2	Sequence 2, Appli
13	37	88.1	9	5	US-10-861-335-1	Sequence 1, Appli
14	37	88.1	9	6	US-11-007-740-20	Sequence 20, Appl
15	37	88.1	10	4	US-10-623-176-43	Sequence 43, Appl
16	37	88.1	13	4	US-10-623-176-76	Sequence 76, Appl
17	37	88.1	13	4	US-10-791-217-16	Sequence 16, Appl
18	37	88.1	13	6	US-11-007-740-28	Sequence 28, Appl
19	36	85.7	9	4	US-10-623-176-1	Sequence 1, Appli
20	36	85.7	9	4	US-10-791-217-1	Sequence 1, Appli
21	36	85.7	9	6	US-11-007-740-29	Sequence 29, Appl
22	36	85.7	10	4	US-10-623-176-24	Sequence 24, Appl
23	34	81.0	9	4	US-10-623-176-48	Sequence 48, Appl
24	33	78.6	9	4	US-10-623-176-23	Sequence 23, Appl
25	33	78.6	9	4	US-10-623-176-41	Sequence 41, Appl
26	33	78.6	9	4	US-10-623-176-45	Sequence 45, Appl
27	33	78.6	10	4	US-10-623-176-7	Sequence 7, Appli
28	33	78.6	13	4	US-10-623-176-64	Sequence 64, Appl
29	29	69.0	9	4	US-10-623-176-5	Sequence 5, Appli
30	29	69.0	9	4	US-10-623-176-47	Sequence 47, Appl
31	29	69.0	14	4	US-10-623-176-62	Sequence 62, Appl
32	28	66.7	9	4	US-10-623-176-40	Sequence 40, Appl
33	28	66.7	10	4	US-10-623-176-6	Sequence 6, Appli
34	28	66.7	13	4	US-10-623-176-54	Sequence 54, Appl
35	27	64.3	10	4	US-10-623-176-8	Sequence 8, Appli
36	26	61.9	10	3	US-09-572-404B-428	Sequence 428, App
37	26	61.9	10	4	US-10-153-344-11	Sequence 11, Appl
38	25	59.5	9	3	US-09-834-765-349	Sequence 349, App
39	25	59.5	9	4	US-10-623-176-39	Sequence 39, Appl
40	25	59.5	10	4	US-10-702-400-90	Sequence 90, Appl
41	25	59.5	10	5	US-10-805-650-90	Sequence 90, Appl
42	24	57.1	7	4	US-10-271-708-16	Sequence 16, Appl
43	24	57.1	9	4	US-10-623-176-4	Sequence 4, Appli
44	24	57.1	9	5	US-10-503-135-26	Sequence 26, Appl
45	24	57.1	9	5	US-10-503-135-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H

```
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

  Query Match             100.0%;  Score 42;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 3
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

  Query Match             100.0%;  Score 42;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 4
US-10-623-176-44
; Sequence 44, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(10)
US-10-623-176-44

  Query Match             100.0%;  Score 42;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 5
US-10-623-176-65
; Sequence 65, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(12)
US-10-623-176-65

  Query Match             100.0%;  Score 42;  DB 4;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          2 VLRDDLLEA 10


RESULT 6
US-10-623-176-74
; Sequence 74, Application US/10623176
; Publication No. US20040092446A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: KIAA0223
;   OTHER INFORMATION: sequence derived from a presumed HA-1 negative
;   OTHER INFORMATION: individual
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(13)
US-10-623-176-74

  Query Match             100.0%;  Score 42;  DB 4;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          3 VLRDDLLEA 11


RESULT 7
US-10-791-217-14
; Sequence 14, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from HA-1-/- phenotype
US-10-791-217-14

  Query Match             100.0%;  Score 42;  DB 4;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          3 VLRDDLLEA 11


RESULT 8
US-11-007-740-26
; Sequence 26, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PCR Product
US-11-007-740-26

  Query Match             100.0%;  Score 42;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          3 VLRDDLLEA 11


RESULT 9
US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-42

  Query Match             90.5%;  Score 38;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              ||||||||
Db          2 VLRDDLLE 9
```

```
RESULT 10
US-10-623-176-46
; Sequence 46, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-46

  Query Match             90.5%;  Score 38;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLLEA 9
              ||||||||
Db          1 LRDDLLEA 8


RESULT 11
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-2

  Query Match             88.1%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 12
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

  Query Match             88.1%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 13
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunor
;  TITLE OF INVENTION:  of tumors
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HA-1 peptide
US-10-861-335-1
```

Query Match 88.1%; Score 37; DB 5; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9
```

RESULT 14
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

Query Match 88.1%; Score 37; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9
```

RESULT 15
US-10-623-176-43
; Sequence 43, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(10)
US-10-623-176-43

Query Match 88.1%; Score 37; DB 4; Length 10;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9
```

Search completed: April 6, 2006, 17:28:45
Job time : 96.6667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 17:24:07 ; Search time 12.6667 Seconds
(without alignments)
22.163 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 65691

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	7	US-11-010-748A-12	Sequence 12, Appl
2	37	88.1	9	7	US-11-010-748A-11	Sequence 11, Appl
3	21	50.0	4	7	US-11-019-027-17	Sequence 17, Appl
4	21	50.0	7	7	US-11-096-706-52	Sequence 52, Appl
5	21	50.0	7	7	US-11-225-686-208	Sequence 208, App
6	21	50.0	7	7	US-11-225-686-211	Sequence 211, App
7	21	50.0	7	7	US-11-225-686-216	Sequence 216, App
8	21	50.0	7	7	US-11-202-009-208	Sequence 208, App
9	21	50.0	7	7	US-11-202-009-211	Sequence 211, App
10	21	50.0	7	7	US-11-202-009-216	Sequence 216, App
11	21	50.0	9	6	US-10-989-767A-219	Sequence 219, App
12	21	50.0	9	6	US-10-989-767A-565	Sequence 565, App
13	21	50.0	10	6	US-10-989-767A-159	Sequence 159, App
14	21	50.0	10	6	US-10-989-767A-268	Sequence 268, App
15	21	50.0	10	6	US-10-989-767A-272	Sequence 272, App
16	21	50.0	10	6	US-10-989-767A-441	Sequence 441, App
17	21	50.0	10	6	US-10-989-767A-547	Sequence 547, App
18	20	47.6	5	7	US-11-129-143-168	Sequence 168, App
19	20	47.6	5	7	US-11-129-143-169	Sequence 169, App
20	20	47.6	5	7	US-11-129-143-170	Sequence 170, App
21	20	47.6	5	7	US-11-129-143-171	Sequence 171, App
22	20	47.6	5	7	US-11-129-143-172	Sequence 172, App
23	20	47.6	5	7	US-11-129-143-173	Sequence 173, App
24	20	47.6	7	6	US-10-982-440-126	Sequence 126, App
25	20	47.6	7	7	US-11-096-706-88	Sequence 88, Appl
26	20	47.6	7	7	US-11-096-706-164	Sequence 164, App
27	20	47.6	8	7	US-11-021-305-62	Sequence 62, Appl
28	20	47.6	8	7	US-11-021-305-65	Sequence 65, Appl
29	20	47.6	8	7	US-11-021-305-66	Sequence 66, Appl
30	20	47.6	9	6	US-10-927-435-63	Sequence 63, Appl
31	20	47.6	9	6	US-10-927-634-63	Sequence 63, Appl
32	20	47.6	10	7	US-11-254-419-60	Sequence 60, Appl
33	20	47.6	10	7	US-11-254-419-67	Sequence 67, Appl
34	20	47.6	12	7	US-11-004-399-1909	Sequence 1909, Ap
35	20	47.6	14	7	US-11-127-677-130	Sequence 130, App
36	20	47.6	15	6	US-10-353-783-71	Sequence 71, Appl
37	20	47.6	15	6	US-10-718-264-162	Sequence 162, App
38	20	47.6	15	6	US-10-718-264-162	Sequence 162, App
39	20	47.6	15	6	US-10-522-297-12	Sequence 12, Appl
40	20	47.6	15	6	US-10-522-297-13	Sequence 13, Appl
41	20	47.6	15	7	US-11-106-932-84	Sequence 84, Appl
42	20	47.6	15	7	US-11-126-841A-8	Sequence 8, Appli
43	20	47.6	15	7	US-11-172-740-1404	Sequence 1404, Ap
44	19	45.2	7	7	US-11-225-686-2954	Sequence 2954, Ap
45	19	45.2	7	7	US-11-225-686-3877	Sequence 3877, Ap

ALIGNMENTS

RESULT 1
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-12

Query Match 100.0%; Score 42; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

```
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
;  FILE REFERENCE: MER-136
;  CURRENT APPLICATION NUMBER: US/11/010,748A
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/EP03/06251
;  PRIOR FILING DATE: 2003-06-13
;  PRIOR APPLICATION NUMBER: EP02013423.5
;  PRIOR FILING DATE: 2002-06-13
;  NUMBER OF SEQ ID NOS: 926
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
;   OTHER INFORMATION: ell epitopes
US-11-010-748A-11

  Query Match             88.1%;  Score 37;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || |||||
Db          1 VLHDDLLEA 9


RESULT 3
US-11-019-027-17
; Sequence 17, Application US/11019027
; Publication No. US20050282181A1
; GENERAL INFORMATION:
;  APPLICANT: YAN, Wei
;  APPLICANT:  SHEN, Wenyan
;  APPLICANT:  ZHOU, Hongxing
;  APPLICANT:  ZHOU, Chen
;  APPLICANT:  COSMAN, David J.
;  APPLICANT:  CARTER, Paul
;  APPLICANT:  MARTIN, Francis H.
;  TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
;  FILE REFERENCE: A-890A
;  CURRENT APPLICATION NUMBER: US/11/019,027
;  CURRENT FILING DATE:  2004-12-21
;  PRIOR APPLICATION NUMBER: 60/605,902
;  PRIOR FILING DATE: 2004-08-31
;  PRIOR APPLICATION NUMBER: 60/531,714
;  PRIOR FILING DATE: 2003-12-22
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: ER localization signal
US-11-019-027-17

  Query Match             50.0%;  Score 21;  DB 7;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDL 6
              ||||
Db          1 RDDL 4


RESULT 4
US-11-096-706-52
; Sequence 52, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
;  APPLICANT: Sangamo Biosciences, Inc.
;  APPLICANT:  Collingwood, Trevor
;  TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
;  FILE REFERENCE: 019496-008220US
;  CURRENT APPLICATION NUMBER: US/11/096,706
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 60/560,535
;  PRIOR FILING DATE: 2004-04-08
;  PRIOR APPLICATION NUMBER: US 60/576,757
;  PRIOR FILING DATE: 2004-06-02
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
;   OTHER INFORMATION: region)
US-11-096-706-52

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDL 6
              ||||
Db          2 RDDL 5


RESULT 5
US-11-225-686-208
; Sequence 208, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/225,686
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-208

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |||:
Db          1 RSDLLQ 6


RESULT 6
US-11-225-686-211
; Sequence 211, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/225,686
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;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-211

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |||:
Db          1 RSDLLQ 6


RESULT 7
US-11-225-686-216
; Sequence 216, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/225,686
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-216

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |||:
Db          1 RSDLLQ 6


RESULT 8
US-11-202-009-208
; Sequence 208, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/202,009
;  CURRENT FILING DATE:  2005-08-11
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-208

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |||:
Db          1 RSDLLQ 6


RESULT 9
US-11-202-009-211
; Sequence 211, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/202,009
;  CURRENT FILING DATE:  2005-08-11
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-211

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |||:
Db          1 RSDLLQ 6


RESULT 10
US-11-202-009-216
; Sequence 216, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/202,009
;  CURRENT FILING DATE:  2005-08-11
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-216

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
```

```
              | |||:
Db          1 RSDLLQ 6


RESULT 11
US-10-989-767A-219
; Sequence 219, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
;  APPLICANT: FARIS, MARY
;  APPLICANT:  HUBERT, RENE
;  APPLICANT:  RAITANO, ARTHUR
;  APPLICANT:  AFAR, DANIEL
;  APPLICANT:  LEVIN, ELANA
;  APPLICANT:  CHALLITA-EID, PIA
;  APPLICANT:  JAKOBOVITZ, AYA
;  TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
;  TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
;  TITLE OF INVENTION:  OTHER CANCERS
;  FILE REFERENCE: 511582005004
;  CURRENT APPLICATION NUMBER: US/10/989,767A
;  CURRENT FILING DATE:  2004-11-15
;  PRIOR APPLICATION NUMBER: 10/277,292
;  PRIOR FILING DATE: 2002-10-21
;  PRIOR APPLICATION NUMBER: 09/935,430
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/227,098
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 60/282,739
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 700
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 219
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-219

  Query Match             50.0%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   37.5%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              ::: ||:|
Db          1 LMKSDLVE 8


RESULT 12
US-10-989-767A-565
; Sequence 565, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
;  APPLICANT: FARIS, MARY
;  APPLICANT:  HUBERT, RENE
;  APPLICANT:  RAITANO, ARTHUR
;  APPLICANT:  AFAR, DANIEL
;  APPLICANT:  LEVIN, ELANA
;  APPLICANT:  CHALLITA-EID, PIA
;  APPLICANT:  JAKOBOVITZ, AYA
;  TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
;  TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
;  TITLE OF INVENTION:  OTHER CANCERS
;  FILE REFERENCE: 511582005004
;  CURRENT APPLICATION NUMBER: US/10/989,767A
;  CURRENT FILING DATE:  2004-11-15
;  PRIOR APPLICATION NUMBER: 10/277,292
;  PRIOR FILING DATE: 2002-10-21
;  PRIOR APPLICATION NUMBER: 09/935,430
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/227,098
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 60/282,739
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 700
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 565
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-565

  Query Match             50.0%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   37.5%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              ::: ||:|
Db          1 LMKSDLVE 8


RESULT 13
US-10-989-767A-159
; Sequence 159, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
;  APPLICANT: FARIS, MARY
;  APPLICANT:  HUBERT, RENE
;  APPLICANT:  RAITANO, ARTHUR
;  APPLICANT:  AFAR, DANIEL
;  APPLICANT:  LEVIN, ELANA
;  APPLICANT:  CHALLITA-EID, PIA
;  APPLICANT:  JAKOBOVITZ, AYA
;  TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
;  TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
;  TITLE OF INVENTION:  OTHER CANCERS
;  FILE REFERENCE: 511582005004
;  CURRENT APPLICATION NUMBER: US/10/989,767A
;  CURRENT FILING DATE:  2004-11-15
;  PRIOR APPLICATION NUMBER: 10/277,292
;  PRIOR FILING DATE: 2002-10-21
;  PRIOR APPLICATION NUMBER: 09/935,430
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/227,098
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 60/282,739
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 700
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-159

  Query Match             50.0%;  Score 21;  DB 6;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 1.7e+02;
  Matches    3;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              :| |: :|:
Db          1 ILNDNAIES 9


RESULT 14
US-10-989-767A-268
; Sequence 268, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
;  APPLICANT: FARIS, MARY
;  APPLICANT:  HUBERT, RENE
```

; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 268
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-268

Query Match 50.0%; Score 21; DB 6; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLE 8
::: ||:|
Db 2 LMKSDLVE 9

RESULT 15
US-10-989-767A-272
; Sequence 272, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-272

Query Match 50.0%; Score 21; DB 6; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLE 8
::: ||:|
Db 1 LMKSDLVE 8

Search completed: April 6, 2006, 17:29:29
Job time : 12.6667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:12:46 ; Search time 111.667 Seconds
(without alignments)
35.413 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	2	AAW99195	Aaw99195 Minor his
2	36	97.3	9	2	AAW99196	Aaw99196 Minor his
3	36	97.3	9	2	AAW99197	Aaw99197 Minor his
4	36	97.3	9	2	AAW97572	Aaw97572 T-cell ep
5	36	97.3	9	2	AAW97375	Aaw97375 HA-1 H-al
6	36	97.3	9	2	AAW97374	Aaw97374 HA-1 R-al
7	36	97.3	9	8	ADH40333	Adh40333 Human min
8	36	97.3	9	8	ADH40334	Adh40334 Human min
9	26	70.3	9	8	ADT73023	Adt73023 Human RSV
10	24	64.9	9	8	ABY01546	Aby01546 SARS coro
11	24	64.9	9	9	ADZ50925	Adz50925 Y. pestis
12	23	62.2	9	5	AAU71211	Aau71211 Human MHC
13	23	62.2	9	5	AAU71428	Aau71428 Human MHC
14	23	62.2	9	8	ADT73690	Adt73690 Human RSV
15	23	62.2	9	8	ADT72767	Adt72767 Human RSV
16	23	62.2	9	8	ABY01413	Aby01413 SARS coro
17	23	62.2	9	9	ADW23047	Adw23047 SARS coro
18	22	59.5	9	3	AAY80162	Aay80162 HLA-A2 re
19	22	59.5	9	5	AAU09449	Aau09449 Chlamydop
20	22	59.5	9	6	ABP75298	Abp75298 Chlamydia
21	22	59.5	9	6	ABP75138	Abp75138 Proteome
22	22	59.5	9	6	ABP75181	Abp75181 Proteome
23	22	59.5	9	8	ADT72766	Adt72766 Human RSV
24	22	59.5	9	8	ADT73689	Adt73689 Human RSV
25	22	59.5	9	8	ADU99853	Adu99853 BCZ4 tumo
26	22	59.5	9	8	ABY01301	Aby01301 SARS coro
27	22	59.5	9	9	ADZ57184	Adz57184 Cytotoxic
28	21	56.8	6	3	AAB12035	Aab12035 Peptide #
29	21	56.8	6	5	AAU80810	Aau80810 Rat Rb-in
30	21	56.8	6	7	ADE84629	Ade84629 Mammalia
31	21	56.8	8	3	AAB12089	Aab12089 Ad7 ce1 p
32	21	56.8	8	7	ADE84662	Ade84662 Adenoviru
33	21	56.8	9	2	AAW47427	Aaw47427 Prenyl di
34	21	56.8	9	2	AAW97373	Aaw97373 Peptide e
35	21	56.8	9	3	AAB12092	Aab12092 Ad40 ce1
36	21	56.8	9	3	AAB12086	Aab12086 Ce1 motif
37	21	56.8	9	4	ABB12506	Abb12506 Human C35
38	21	56.8	9	4	ABB13927	Abb13927 Human C35
39	21	56.8	9	4	ABB12554	Abb12554 Human C35
40	21	56.8	9	4	ABB13072	Abb13072 Human C35
41	21	56.8	9	4	ABB13115	Abb13115 Human C35
42	21	56.8	9	4	ABB13184	Abb13184 Human C35
43	21	56.8	9	4	ABB13867	Abb13867 Human C35
44	21	56.8	9	4	ABB14131	Abb14131 Human C35
45	21	56.8	9	4	ABB12498	Abb12498 Human C35

ALIGNMENTS

RESULT 1
AAW99195
ID AAW99195 standard; peptide; 9 AA.
XX
AC AAW99195;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /label= His, Arg
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 1; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the

```
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 2
AAW99196
ID   AAW99196 standard; peptide; 9 AA.
XX
AC   AAW99196;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Claim 3; Page 32; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 3
AAW99197
ID   AAW99197 standard; peptide; 9 AA.
XX
AC   AAW99197;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Disclosure; Page 15; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 4
AAW97572
ID   AAW97572 standard; peptide; 9 AA.
XX
AC   AAW97572;
XX
DT   20-MAY-1999  (first entry)
XX
DE   T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW   T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW   transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW   neoplastic haematopoietic cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /note= "His or Arg"
XX
```

PN WO9905173-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000424.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-142855/12.
XX
PT Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT for inducing tolerance to transplants and prevent rejection or graft-
PT versus-host disease.
XX
PS Claim 1; Page 39; 57pp; English.
XX
CC The present sequence represents an immunogenic peptide constituting a T-
CC cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC The peptide can be used in vaccines or pharmaceutical formulations as
CC medicines to induce tolerance for transplants so as to prevent rejection
CC and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC I context, can be eliminated after specific recognition of the peptides.
CC The peptides can also be used to raise antibodies, T-cell receptor, B-
CC and T-cells
XX
SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|||||||||
Db 1 VLXDDLLEA 9

RESULT 5
AAW97375
ID AAW97375 standard; protein; 9 AA.
XX
AC AAW97375;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 H-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 18; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 H-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC anti-idiotypic B cells and/or T cells and antibodies
XX
SQ Sequence 9 AA;

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 6
AAW97374
ID AAW97374 standard; protein; 9 AA.
XX
AC AAW97374;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 R-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 13; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 R-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used

```
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
ADH40333
ID   ADH40333 standard; peptide; 9 AA.
XX
AC   ADH40333;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 8
ADH40334
ID   ADH40334 standard; peptide; 9 AA.
XX
AC   ADH40334;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             97.3%;  Score 36;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 9
ADT73023
ID   ADT73023 standard; peptide; 9 AA.
```

XX
AC ADT73023;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 919.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 16; SEQ ID NO 919; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 70.3%; Score 26; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 VLXDDLLEA 9
              :: ||:| |
Db          1 IIKDDILSA 9
```

RESULT 10
ABY01546
ID ABY01546 standard; peptide; 9 AA.
XX
AC ABY01546;
XX
DT 16-JUN-2005 (first entry)
XX
DE SARS coronavirus spike protein HLA A 0201 T-cell epitope, SEQ:8174.
XX
KW Vaccine; nucleic acid vaccine; drug screening; diagnosis;
KW SARS coronavirus infection; infection; respiratory disease; virucide.
XX
OS SARS coronavirus.
XX
PN WO2004092360-A2.
XX
PD 28-OCT-2004.
XX
PF 09-APR-2004; 2004WO-US011710.
XX
PR 10-APR-2003; 2003US-0462218P.
PR 11-APR-2003; 2003US-0462465P.
PR 12-APR-2003; 2003US-0462418P.
PR 13-APR-2003; 2003US-0462748P.
PR 14-APR-2003; 2003US-0463109P.
PR 15-APR-2003; 2003US-0463460P.
PR 16-APR-2003; 2003US-0463668P.
PR 17-APR-2003; 2003US-0463983P.
PR 18-APR-2003; 2003US-0463971P.
PR 22-APR-2003; 2003US-0464838P.
PR 22-APR-2003; 2003US-0464899P.
PR 23-APR-2003; 2003US-0465273P.
PR 24-APR-2003; 2003US-0465535P.
PR 05-MAY-2003; 2003US-0468312P.
PR 22-MAY-2003; 2003US-0473144P.
PR 14-AUG-2003; 2003US-0495024P.
PR 23-SEP-2003; 2003US-0505652P.
PR 11-OCT-2003; 2003US-0510781P.
PR 11-DEC-2003; 2003US-0529464P.
PR 12-JAN-2004; 2004US-0536177P.
PR 07-APR-2004; 2004US-0560757P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Rappuoli R, Masignani V, Stadler K, Gregersen J, Chien D, Han J;
PI Polo J, Weiner A, Houghton M, Song HC, Seo MY, Donnelly JJ;
PI Klenk HD, Valiante N;
XX
DR WPI; 2004-766863/75.
XX
PT Novel isolated polypeptide e.g. spike polypeptide, Env polypeptide, of
PT severe acute respiratory syndrome virus (SARS), useful as vaccine for
PT SARS.
XX
PS Disclosure; SEQ ID NO 8174; 839pp; English.
XX
CC The invention relates to isolated polypeptides of the severe acute
CC respiratory syndrome (SARS) coronavirus. The polypeptides include spike
CC (S or E2), env (E or sM), membrane (M or E1), hemagglutinin-esterase (HE
CC or E3), and nucleocapsid (N) polypeptides, and the ORF1a and ORF1ab
CC (replicase) polypeptides and their proteolytic fragments. The invention
CC also relates to antibodies which recognise the polypeptides; nucleic
CC acids encoding the SARS virus polypeptides; primers specific for SARS
CC virus nucleic acid sequences; kits for amplifying SARS virus target
CC nucleic acids; a double-stranded RNA molecule 10-30 nucleotides in length
CC which is able to inactivate the SARS virus in a mammalian cell; an
CC expression construct for recombinant expression of a SARS virus spike
CC protein; a viral vector for in vivo delivery of a SARS virus polypeptide-
CC encoding nucleic acid; and a mammalian cell line stably expressing a SARS
CC viral antigen. The invention additionally provides a vaccine for the
CC treatment or prevention of SARS comprising an inactivated SARS virus, a
CC killed SARS virus, an attenuated SARS virus, a split SARS virus
CC preparation, or at least one purified SARS virus antigens; methods of
CC making inactivated SARS virus and vaccines containing it; an alpha-virus
CC replicon particle comprising one or more SARS viral antigens; and a
CC vaccine comprising one or more SARS virus antigens and one or more
CC respiratory virus antigens. The invention further encompasses a method of
CC identifying a therapeutically active agent by measuring the effect of the
CC agent on a SARS-related enzyme, and a method of treating a SARS patient
CC using small molecule viral inhibitors. The SARS virus polypeptides and
CC nucleic acids can be used in the preparation and manufacture of vaccines

```
CC   for the treatment or prevention of SARS. The SARS virus polypeptides,
CC   antibodies against them, and SARS virus-specific primers and kits
CC   containing them are useful for diagnosing or identifying the presence of
CC   SARS in a biological sample. The present sequence represents a SARS
CC   coronavirus T-cell epitope. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 9 AA;

  Query Match             64.9%;  Score 24;  DB 8;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 2e+06;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              :| ||:: |
Db          1 LLTDDMIAA 9


RESULT 11
ADZ50925
ID   ADZ50925 standard; peptide; 9 AA.
XX
AC   ADZ50925;
XX
DT   14-JUL-2005  (first entry)
XX
DE   Y. pestis cytotoxic T-cell epitope SEQ ID 993.
XX
KW   Yersinia pestis infection; antibacterial; infection; epitope; T-cell;
KW   vaccine; biological warfare.
XX
OS   Yersinia pestis.
XX
PN   WO2005037855-A2.
XX
PD   28-APR-2005.
XX
PF   15-OCT-2004; 2004WO-US033883.
XX
PR   17-OCT-2003; 2003US-0511653P.
XX
PA   (PECO-) PECOS LABS INC.
XX
PI   Lund O,  Lundegaard C,  Nielsen M,  Worning P,  Deans RJ,  Buus S;
PI   Brunak S;
XX
DR   WPI; 2005-315677/32.
XX
PT   New cytotoxic Yersinia pestis T-cell epitope comprising 10 amino acids,
PT   useful as a vaccine or diagnostic tool and for inducing immune response
PT   in a subject.
XX
PS   Claim 1; SEQ ID NO 993; 235pp; English.
XX
CC   The invention relates to a cytotoxic Yersinia pestis T-cell epitope,
CC   selected from any of the 1000 sequences of 9 amino acids appearing as
CC   ADZ49933-ADZ50932. Also included are predicting peptides that are
CC   epitopes or can be used as diagnostic tools (comprising predicting which
CC   peptides bind to a HMC molecule (not defined) with high affinity using a
CC   neural network with at least one of the following features: some or all
CC   of the inputs to the neural networks are generated using a hidden Markov
CC   model; or some or all of the inputs are encoded by an amino acid
CC   substitution matrix, different from an identity matrix)and a vaccine or
CC   diagnostic tool using a limited number such as at least 1, 2, 3, 4, 5, 8,
CC   16, 32, 64, 128, 256, 512 of the peptides of ADZ49933-ADZ50932. In
CC   predicting peptides, the prediction of the neural network is combined
CC   with prediction or measurement of one of the following: proteasomal
CC   cleavage sites; MHC binding; presence of sequence or related sequence(s)
CC   in patent databases; TAP binding; gene or protein expression level;
CC   function of the protein; localization of the protein; and similarity to
CC   self proteins. The epitope is useful as a vaccine or diagnostic tool, and
CC   for inducing immune response in a subject (said immunity to yersinia
CC   pestis infection, the causative agent of plague). The present sequence is
CC   a cytotoxic Yersinia pestis T-cell epitope of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             64.9%;  Score 24;  DB 9;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 2e+06;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              :| || ||
Db          1 LLLDDALE 8


RESULT 12
AAU71211
ID   AAU71211 standard; peptide; 9 AA.
XX
AC   AAU71211;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human MHC class I molecule HLA-A2 binding 103P3E8 peptide #18.
XX
KW   103P3E8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
KW   tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW   single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW   chromosome 9q13-q21.
XX
OS   Homo sapiens.
XX
PN   WO200179557-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US012181.
XX
PR   12-APR-2000; 2000US-0196647P.
XX
PA   (UROG-) UROGENESYS INC.
XX
PI   Faris M,  Challita-Eid PM,  Raitano AB,  Mitchell SC,  Afar DEH;
PI   Jakobovits A;
XX
DR   WPI; 2002-061976/08.
XX
PT   Monitoring 103P3E8 gene products in sample from patient (suspected of)
PT   having cancer, useful for diagnosing, managing or treating cancers, e.g.
PT   prostate cancer, comprises determining presence of aberrant 103P3E8 gene
PT   products.
XX
PS   Disclosure; Page 84; 128pp; English.
XX
CC   Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and
CC   peptide fragments of the protein. 103P3E8 exhibits tissue specific
CC   expression in normal adult tissue, but it is also aberrantly expressed in
CC   many cancers including tumours of the prostate, bladder, kidney, colon,
CC   lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related
CC   protein and peptide fragments and specific PCR primers are therefore
CC   useful for diagnosing and treating cancer. A vector comprising a
CC   polynucleotide which encodes a single chain monoclonal antibody, that
CC   immunospecifically binds to an 103P3E8-related protein, and a ribozyme
CC   capable of cleaving a polynucleotide having the 103P3E8 coding sequence,
CC   are both useful in the preparation of a composition for treating a
CC   patient with a cancer that expresses 103P3E8. The sequences can be used
CC   in diagnostic methods to monitor the level of 103P3E8 gene products in
CC   serum, blood, urine and tissue and to thereby detect the presence of
CC   cancerous cells
XX
SQ   Sequence 9 AA;

  Query Match             62.2%;  Score 23;  DB 5;  Length 9;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              |||||
Db          1 DLLEA 5


RESULT 13
AAU71428
ID   AAU71428 standard; peptide; 9 AA.
XX
AC   AAU71428;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human MHC molecule HLA-A11 binding 103P3E8 peptide #35.
XX
KW   103P3E8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
KW   tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW   single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW   chromosome 9q13-q21.
XX
OS   Homo sapiens.
XX
PN   WO200179557-A2.
XX
PD   25-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US012181.
XX
PR   12-APR-2000; 2000US-0196647P.
XX
PA   (UROG-) UROGENESYS INC.
XX
PI   Faris M,  Challita-Eid PM,  Raitano AB,  Mitchell SC,  Afar DEH;
PI   Jakobovits A;
XX
DR   WPI; 2002-061976/08.
XX
PT   Monitoring 103P3E8 gene products in sample from patient (suspected of)
PT   having cancer, useful for diagnosing, managing or treating cancers, e.g.
PT   prostate cancer, comprises determining presence of aberrant 103P3E8 gene
PT   products.
XX
PS   Disclosure; Page 90; 128pp; English.
XX
CC   Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and
CC   peptide fragments of the protein. 103P3E8 exhibits tissue specific
CC   expression in normal adult tissue, but it is also aberrantly expressed in
CC   many cancers including tumours of the prostate, bladder, kidney, colon,
CC   lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related
CC   protein and peptide fragments and specific PCR primers are therefore
CC   useful for diagnosing and treating cancer. A vector comprising a
CC   polynucleotide which encodes a single chain monoclonal antibody, that
CC   immunospecifically binds to an 103P3E8-related protein, and a ribozyme
CC   capable of cleaving a polynucleotide having the 103P3E8 coding sequence,
CC   are both useful in the preparation of a composition for treating a
CC   patient with a cancer that expresses 103P3E8. The sequences can be used
CC   in diagnostic methods to monitor the level of 103P3E8 gene products in
CC   serum, blood, urine and tissue and to thereby detect the presence of
CC   cancerous cells
XX
SQ   Sequence 9 AA;

  Query Match             62.2%;  Score 23;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              |||||
Db          5 DLLEA 9


RESULT 14
ADT73690
ID   ADT73690 standard; peptide; 9 AA.
XX
AC   ADT73690;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human RSV L high affinity binding peptide SeqID 1586.
XX
KW   human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW   MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS   Human respiratory syncytial virus.
XX
PN   WO2004092207-A2.
XX
PD   28-OCT-2004.
XX
PF   16-APR-2004; 2004WO-EP004061.
XX
PR   16-APR-2003; 2003EP-00447095.
XX
PA   (ALGO-) ALGONOMICS NV.
XX
PI   Lasters I,  Desmet J,  Stegmann T;
XX
DR   WPI; 2004-758334/74.
XX
PT   New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT   or P) for inducing an immune response to RSV or for diagnosing,
PT   preventing or treating viral infections, particularly RSV infection.
XX
PS   Claim 16; SEQ ID NO 1586; 143pp; English.
XX
CC   This invention relates to novel isolated or purified peptides of the
CC   human respiratory syncytial virus (RSV), in particular ten RSV genes
CC   encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC   known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC   eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC   SH (also known as the 1A protein). Specifically, it refers to a
CC   composition comprising an above peptide mixed with a pharmaceutical
CC   excipient or an RSV immunogenic composition comprising a recombinant
CC   expression vector with a nucleic acid insert encoding an above peptide.
CC   The present invention describes an in vitro method of detecting cytotoxic
CC   T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC   (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC   RSV peptide is useful for preparing a diagnostic composition or an RSV
CC   (prophylactic or therapeutic) vaccine composition for a DNA-based
CC   immunisation, or for preparing an immune response provoking vaccine in
CC   the event of RSV infection (the vaccine being prepared by contacting the
CC   polypeptide in an immune response-provoking amount of specific CTL).
CC   Accordingly, these peptide compositions have virucidal activity. This
CC   peptide sequence is a human RSV high binding affinity peptide of the
CC   invention.
XX
SQ   Sequence 9 AA;

  Query Match             62.2%;  Score 23;  DB 8;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 2e+06;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              :: ||:| |
Db          1 IIKDDILLA 9


RESULT 15
ADT72767
ID   ADT72767 standard; peptide; 9 AA.
XX
AC   ADT72767;
```

XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 663.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Disclosure; SEQ ID NO 663; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 62.2%; Score 23; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 2e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 LXDDLLEA 9
              : ||:| |
Db          1 IKDDILSA 8
```

Search completed: April 6, 2006, 16:19:09
Job time : 113.667 secs

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:19:36 ; Search time 18.6667 Seconds
(without alignments)
46.390 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	43.2	7	2	S68004	hucolin, 75K chain
2	16	43.2	8	2	PC4131	hypothetical prote
3	14	37.8	7	2	S20446	elastase - Pseudom
4	14	37.8	7	2	A59489	protein kinase C i
5	13	35.1	8	2	A61328	trypsin (EC 3.4.21
6	13	35.1	9	2	PH0942	T-cell receptor be
7	13	35.1	9	2	A60427	macrophage cytotox
8	12	32.4	4	2	I40697	biotin A - Citroba
9	12	32.4	5	2	PT0679	T-cell receptor be
10	12	32.4	5	2	PT0601	T-cell receptor be
11	12	32.4	6	2	B35640	cerebellar degener
12	12	32.4	6	2	PT0533	T-cell receptor be
13	12	32.4	7	2	A34026	acetylcholinestera
14	12	32.4	7	2	B39040	calsequestrin, fas
15	12	32.4	7	2	PT0628	T-cell receptor be
16	12	32.4	7	2	PT0722	T-cell receptor be
17	12	32.4	7	2	PT0576	T-cell receptor be
18	12	32.4	8	2	PT0557	T-cell receptor be
19	12	32.4	9	2	PH0108	late G1-69 protein
20	12	32.4	9	2	PT0562	T-cell receptor be
21	12	32.4	9	2	B30572	T-cell receptor be
22	12	32.4	9	2	PS0253	glycine cleavage s
23	11	29.7	6	2	T11779	phosphoglycerate t
24	11	29.7	7	2	S25266	pilE protein - Esc
25	11	29.7	8	2	S22428	chitin-binding pro
26	11	29.7	8	2	B33099	158K exoantigen -
27	11	29.7	8	2	S69165	ferredoxin a2 - Ja
28	11	29.7	9	2	S66419	tetrameric protein
29	11	29.7	9	2	PW0002	chlorophyll a/b-bi
30	11	29.7	9	2	A12872	transaldolase (EC
31	11	29.7	9	2	A61386	macrophage inhibit
32	10	27.0	4	2	A48360	gamma subunit of P
33	10	27.0	4	2	A26209	protein-glutamine
34	10	27.0	6	2	H48394	glycoprotein compo
35	10	27.0	6	2	I48126	alpha-tubulin - Ch
36	10	27.0	7	2	S78024	ribosomal protein
37	10	27.0	7	2	A12016	formylglycinamide
38	10	27.0	7	2	C56793	platelet glycoprot
39	10	27.0	7	2	S29735	polyphosphate-gluc
40	10	27.0	7	2	PC2370	probable H+-transp
41	10	27.0	7	2	T09512	NADH2 dehydrogenas
42	10	27.0	8	2	A32523	peptidyl-dipeptida
43	10	27.0	8	2	T10077	hypothetical prote
44	10	27.0	8	2	PT0298	Ig heavy chain CRD
45	10	27.0	8	2	A42057	fibroblast growth

ALIGNMENTS

RESULT 1
S68004
hucolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>
A;Cross-references: UNIPARC:UPI000017C164

Query Match 43.2%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
|||
Db 4 DDL 6

RESULT 2
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: PC4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding
y for biosynthesis of heme d1.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
A;Accession: PC4131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <KAW>
A;Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:g1217594
A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
C;Superfamily: Pseudomonas stutzeri nirD protein

Query Match 43.2%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
|||
Db 2 DDL 4

```
RESULT 3
S20446
elastase - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C;Accession: S20446
R;Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291-293, 1992
A;Title: Identification of cleavage sites involved in proteolytic processing of Pseudomo
A;Reference number: S20446; MUID:92183956; PMID:1544509
A;Accession: S20446
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <KES>
A;Cross-references: UNIPARC:UPI000017A95F

  Query Match             37.8%;  Score 14;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              ||::
Db          3 DLID 6


RESULT 4
A59489
protein kinase C inhibitor - rat (fragment)
C;Species: Rattus norvegicus
C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C;Accession: A59489
R;Negoro, M.
submitted to the Protein Sequence Database, June 2003
A;Description: Purification of PKCI from rat liver.
A;Reference number: A59489
A;Accession: A59489
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NEG>
A;Experimental source: strain Wistar, liver
A;Note: p-Hydroxyacetophenone-Sepharose binding protein

  Query Match             37.8%;  Score 14;  DB 2;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDD 5
              :  ||
Db          2 IFEDD 6


RESULT 5
A61328
trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C;Accession: A61328
R;Bricteux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema, J
Biochim. Biophys. Acta 386, 244-255, 1975
A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaenop
creas.
A;Reference number: A61328; MUID:75146765; PMID:1125273
A;Accession: A61328
A;Molecule type: protein
A;Residues: 1-8 <BRI>
A;Cross-references: UNIPROT:Q7M390; UNIPARC:UPI000017C43F
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-8/Domain: activation peptide #status experimental <APT>

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDD 5
              : ||
Db          3 IDDD 6


RESULT 6
PH0942
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0942
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0942
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Cross-references: UNIPARC:UPI000017C9DD
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon TGC for residue 2 as Ala
C;Keywords: T-cell receptor

  Query Match             35.1%;  Score 13;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 LLE 8
              |||
Db          5 LLE 7


RESULT 7
A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60427
R;Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin
A;Reference number: A60427; MUID:91372335; PMID:1909970
A;Accession: A60427
A;Molecule type: protein
A;Residues: 1-9 <JON>
A;Cross-references: UNIPROT:Q7M4R5; UNIPARC:UPI0000142BE0
A;Note: the sequence from the text on page 706 is inconsistent with that from page 708 i
C;Keywords: cytokine

  Query Match             35.1%;  Score 13;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXD 4
              || |
Db          4 VLED 7


RESULT 8
I40697
biotin A - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40697
R;Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A;Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacte
A;Reference number: I40697; MUID:89006280; PMID:2971595
A;Accession: I40697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
```

A;Cross-references: UNIPROT:P13071; UNIPARC:UPI000017AA21; GB:M21922; NID:g144434

Query Match 32.4%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 3 DD 4

RESULT 9
PT0679
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0679
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPARC:UPI000017C84D
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
A;Accession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C84D
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 4 DD 5

RESULT 10
PT0601
T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0601; PT0617; PT0694
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0601
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPROT:Q64512; UNIPARC:UPI000017C7E6
A;Experimental source: newborn thymus, strain BALB/c, clone 120-2K
A;Accession: PT0617
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Cross-references: UNIPARC:UPI000017C7E6
A;Experimental source: newborn thymus, strain BALB/c, 120-2CA
A;Accession: PT0694
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C7E6
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H
C;Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 4 DD 5

RESULT 11
B35640
cerebellar degeneration-related protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C;Accession: B35640
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal ma
A;Reference number: A35640; MUID:90222173; PMID:2326268
A;Accession: B35640
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6 <CHE>
A;Cross-references: UNIPARC:UPI000017C63A

Query Match 32.4%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
:||
Db 3 EDL 5

RESULT 12
PT0533
T-cell receptor beta chain V-D-J region (126-1AA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0533
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0533
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C801
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 32.4%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 4 DD 5

RESULT 13
A34026
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C;Accession: A34026
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.; '
J. Biol. Chem. 263, 1140-1145, 1988
A;Title: Divergence in primary structure between the molecular forms of acetylcholineste
A;Reference number: A34026; MUID:88087239; PMID:3335534
A;Accession: A34026

```
A;Molecule type: protein
A;Residues: 1-7 <GIB>
A;Cross-references: UNIPARC:UPI000017BF32
C;Keywords: alternative splicing; carboxylic ester hydrolase

  Query Match             32.4%;  Score 12;  DB 2;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 LLEA 9
              || |
Db          1 LLNA 4


RESULT 14
B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein
A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: B39040
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <CAL>
A;Cross-references: UNIPARC:UPI000017C5BC
C;Keywords: phosphoprotein; skeletal muscle

  Query Match             32.4%;  Score 12;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DD 5
              ||
Db          1 DD 2


RESULT 15
PT0628
T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0628
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Cross-references: UNIPARC:UPI000017C7CD
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

  Query Match             32.4%;  Score 12;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DD 5
              ||
Db          4 DD 5


Search completed: April  6, 2006, 16:26:10
Job time : 20.6667 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:13:46 ; Search time 118 Seconds
(without alignments)
53.811 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	43.2	9	2	Q70SM2_HUMAN	Q70sm2 homo sapien
2	16	43.2	9	2	Q8LPT5_MAIZE	Q8lpt5 zea mays (m
3	16	43.2	9	2	P82568_STRPY	P82568 streptococc
4	15	40.5	9	2	Q9XJN0_9VIRU	Q9xjn0 bacteriopha
5	14	37.8	9	2	Q9FSZ2_CICAR	Q9fsz2 cicer ariet
6	14	37.8	9	2	Q9QZA8_MOUSE	Q9qza8 mus musculu
7	14	37.8	9	2	Q85710_9RETR	Q85710 rous sarcom
8	14	37.8	9	2	Q8UTD7_9HIV1	Q8utd7 human immun
9	13	35.1	7	2	O99182_9SMEG	O99182 gnatholebia
10	13	35.1	8	2	Q6U7R2_CRYNV	Q6u7r2 cryptococcu
11	13	35.1	8	2	Q9HDS4_ASPFL	Q9hds4 aspergillus
12	13	35.1	8	2	Q7M390_BALAC	Q7m390 balaenopter
13	13	35.1	8	2	Q8H9K1_9CAUD	Q8h9k1 bacteriopha
14	13	35.1	8	2	Q8SBJ0_BPR69	Q8sbj0 bacteriopha
15	13	35.1	8	2	Q6JC68_SOYBN	Q6jc68 glycine max
16	13	35.1	8	2	P72279_RHOGO	P72279 rhodococcus
17	13	35.1	8	2	Q51594_9ZZZZ	Q51594 plasmid col
18	13	35.1	9	2	Q7M4R5_HUMAN	Q7m4r5 homo sapien
19	13	35.1	9	2	Q9BQT4_HUMAN	Q9bqt4 homo sapien
20	13	35.1	9	2	Q6UVK2_MALDO	Q6uvk2 malus domes
21	13	35.1	9	2	Q56SS9_SAMCA	Q56ss9 sambucus ca
22	13	35.1	9	2	Q56ST0_9DIPS	Q56st0 viburnum ut
23	13	35.1	9	2	Q56ST1_9DIPS	Q56st1 viburnum ur
24	13	35.1	9	2	Q56ST2_9DIPS	Q56st2 viburnum tr
25	13	35.1	9	2	Q56ST3_VIBOP	Q56st3 viburnum op
26	13	35.1	9	2	Q56ST4_9DIPS	Q56st4 viburnum ti
27	13	35.1	9	2	Q56ST5_9DIPS	Q56st5 viburnum su
28	13	35.1	9	2	Q56ST6_9DIPS	Q56st6 viburnum st
29	13	35.1	9	2	Q56ST7_9DIPS	Q56st7 viburnum si
30	13	35.1	9	2	Q56ST8_9DIPS	Q56st8 viburnum sa
31	13	35.1	9	2	Q56ST9_9DIPS	Q56st9 viburnum ru
32	13	35.1	9	2	Q56SU1_9DIPS	Q56su1 viburnum pr
33	13	35.1	9	2	Q56SU2_9DIPS	Q56su2 viburnum pl
34	13	35.1	9	2	Q56SU3_9DIPS	Q56su3 viburnum od
35	13	35.1	9	2	Q56SU4_9DIPS	Q56su4 viburnum nu
36	13	35.1	9	2	Q56SU5_9DIPS	Q56su5 viburnum mo
37	13	35.1	9	2	Q56SU6_9DIPS	Q56su6 viburnum me
38	13	35.1	9	2	Q56SU7_9DIPS	Q56su7 viburnum lo
39	13	35.1	9	2	Q56SU8_9DIPS	Q56su8 viburnum le
40	13	35.1	9	2	Q56SU9_VIBLN	Q56su9 viburnum la
41	13	35.1	9	2	Q56SV0_VIBLA	Q56sv0 viburnum la
42	13	35.1	9	2	Q56SV1_9DIPS	Q56sv1 viburnum ka
43	13	35.1	9	2	Q56SV2_9DIPS	Q56sv2 viburnum ju
44	13	35.1	9	2	Q56SV3_9DIPS	Q56sv3 viburnum ja
45	13	35.1	9	2	Q56SV4_9DIPS	Q56sv4 viburnum ha

ALIGNMENTS

RESULT 1
Q70SM2_HUMAN
ID Q70SM2_HUMAN PRELIMINARY; PRT; 9 AA.
AC Q70SM2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypermethylated in cancer 1 (Fragment).
GN Name=HIC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Pinte S., Guerardel C., Deltour S., Godwin A.K., Leprince D.;
RT "Identification of a second G-C-rich promoter conserved in the human,
RT murine and rat tumor suppressor genes HIC1.";
RL Oncogene 23:4023-4031(2004).
DR EMBL; AJ550616; CAD79467.1; -; mRNA.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 964 MW; 5B5E6DDB1681AAA7 CRC64;

Query Match 43.2%; Score 16; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          5 DLLEA 9
              | :||
Db          3 DTMEA 7
```

RESULT 2
Q8LPT5_MAIZE
ID Q8LPT5_MAIZE PRELIMINARY; PRT; 9 AA.
AC Q8LPT5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-expansin-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY094310; AAM21836.1; -; Genomic_DNA.
FT NON_TER 1 1

```
SQ   SEQUENCE   9 AA;  977 MW;  5C05B2D2CB1AAAA3 CRC64;

  Query Match             43.2%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              |::::|
Db          4 DEVVDA 9


RESULT 3
P82568_STRPY
ID   P82568_STRPY  PRELIMINARY;      PRT;     9 AA.
AC   P82568;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Unknown protein from 2D-page (Fragment).
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC   STRAIN=JRS4;
RA   Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA   VanBogelen R.A.;
RT   "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT   proteins.";
RL   Submitted (MAY-2000) to Swiss-Prot.
CC   -!- MASS SPECTROMETRY: MW=22592.04; METHOD=Electrospray.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1069 MW;  2A771042CB1AB2D7 CRC64;

  Query Match             43.2%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              |:::|
Db          4 DEVIE 8


RESULT 4
Q9XJN0_9VIRU
ID   Q9XJN0_9VIRU PRELIMINARY;      PRT;     9 AA.
AC   Q9XJN0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P10 (Fragment).
OS   Bacteriophage phi-10.
OC   Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
OX   NCBI_TaxID=90889;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99350412; PubMed=10419946;
RA   Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
RA   Hoogstraten D.;
RT   "Isolation of additional bacteriophages with genomes of segmented
RT   double-stranded RNA.";
RL   J. Bacteriol. 181:4505-4508(1999).
DR   EMBL; AF125675; AAD22555.1; -; Genomic_RNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1058 MW;  880E376AA720544A CRC64;

  Query Match             40.5%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              |::|:
Db          2 DNILD 6


RESULT 5
Q9FSZ2_CICAR
ID   Q9FSZ2_CICAR PRELIMINARY;      PRT;     9 AA.
AC   Q9FSZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Cicer arietinum (Chickpea) (Garbanzo).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
OX   NCBI_TaxID=3827;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Etiolated epicotyls;
RA   Dopico B., Jimenez T., Labrador E.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ299069; CAC10216.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  990 MW;  9441BDDAA7272EBE CRC64;

  Query Match             37.8%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 LLEA 9
              ||:|
Db          4 LLDA 7


RESULT 6
Q9QZA8_MOUSE
ID   Q9QZA8_MOUSE PRELIMINARY;      PRT;     9 AA.
AC   Q9QZA8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C-type lectin DCL1 (Fragment).
GN   Name=Clec2i; Synonyms=Dcl1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF192526; AAF04843.1; -; Genomic_DNA.
DR   MGI; MGI:2136650; Clec2i.
DR   MGI; MGI:2136650; Dcl1.
DR   GO; GO:0009897; C:external side of plasma membrane; IDA.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0046703; F:natural killer cell lectin-like receptor bi. . .; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); TAS.
KW   Lectin.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  994 MW;  342161AB172EBAB7 CRC64;

  Query Match             37.8%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              | ||
Db          3 DCLE 6
```

```
RESULT 7
Q85710_9RETR
ID   Q85710_9RETR PRELIMINARY;      PRT;     9 AA.
AC   Q85710;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Pol protein (Fragment).
OS   Rous sarcoma virus.
OC   Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX   NCBI_TaxID=11886;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84115080; PubMed=6319754;
RA   Lerner T.L., Hanafusa H.;
RT   "DNA sequence of the Bryan high-titer strain of Rous sarcoma virus:
RT   extent of env deletion and possible genealogical relationship with
RT   other viral strains.";
RL   J. Virol. 49:549-556(1984).
DR   EMBL; K03365; AAA42557.1; -; Genomic_RNA.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  949 MW;  94AA144DDDD731AA CRC64;

  Query Match             37.8%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              :| | |
Db          1 EDTLAA 6


RESULT 8
Q8UTD7_9HIV1
ID   Q8UTD7_9HIV1 PRELIMINARY;      PRT;     9 AA.
AC   Q8UTD7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Vpu protein.
GN   Name=vpu;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC   Primate lentivirus group.
OX   NCBI_TaxID=11676;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21988475; PubMed=11991972;
RX   DOI=10.1128/JVI.76.11.5435-5451.2002;
RA   Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
RA   Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,
RA   Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
RA   Marlink R., Lee T.-H., Essex M.;
RT   "Human immunodeficiency virus type 1 subtype C molecular phylogeny:
RT   consensus sequence for an AIDS vaccine design?";
RL   J. Virol. 76:5435-5451(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Novitsky V.A., McLane M.F., Chigwedere P., Ndung'u T., Klein I.,
RA   Chang S.-Y., Peter T., Thior I., Rybak N., Gaseitsiwe S., Vannberg F.,
RA   Marlink R., Lee T.-H., Essex M.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF443091; AAL34712.1; -; Genomic_DNA.
SQ   SEQUENCE   9 AA;  1102 MW;  188BD40B17272440 CRC64;

  Query Match             37.8%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              :|||
Db          3 NLLE 6


RESULT 9
O99182_9SMEG
ID   O99182_9SMEG PRELIMINARY;      PRT;     7 AA.
AC   O99182;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytochrome oxidase I (Fragment).
GN   Name=COI;
OS   Gnatholebias zonatus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX   NCBI_TaxID=135316;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA   Murphy W.J., Thomerson J.E., Collier G.E.;
RT   "Phylogeny of the Neotropical killifish family Rivulidae
RT   (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT   sequences.";
RL   Mol. Phylogenet. Evol. 13:289-301(1999).
DR   EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  899 MW;  672721F6CB572030 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VLXDDLL 7
              :|  ||
Db          1 ILYQHLL 7


RESULT 10
Q6U7R2_CRYNV
ID   Q6U7R2_CRYNV PRELIMINARY;      PRT;     8 AA.
AC   Q6U7R2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Squalene monooxygenase (EC 1.14.99.7) (Fragment).
GN   Name=ERG1;
OS   Cryptococcus neoformans var. grubii H99.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=235443;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=H99;
RA   Stuart L.T., Allen A., Dietrich F.S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY376718; AAQ88127.1; -; mRNA.
DR   GO; GO:0004506; F:squalene monooxygenase activity; IEA.
KW   Monooxygenase; Oxidoreductase.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  811 MW;  0467776AAB1DD727 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDD 5
              :| :|
Db          1 LLAED 5
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RESULT 11
Q9HDS4_ASPFL
ID   Q9HDS4_ASPFL PRELIMINARY;      PRT;     8 AA.
AC   Q9HDS4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   TrpC polyprotein (Fragment).
GN   Name=trpC;
OS   Aspergillus flavus.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5059;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=A55;
RX   MEDLINE=21173963; PubMed=11273679; DOI=10.1006/fgbi.2000.1215;
RA   Geiser D.M., Dorner J.W., Horn B.W., Taylor J.W.;
RT   "The phylogenetics of mycotoxin and sclerotium production in
RT   Aspergillus flavus and Aspergillus oryzae.";
RL   Fungal Genet. Biol. 31:169-179(2000).
DR   EMBL; AF261861; AAG16135.1; -; Genomic_DNA.
KW   Polyprotein.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  807 MW;  F3B2C72AB5B87DD6 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              ||::
Db          5 DLVD 8


RESULT 12
Q7M390_BALAC
ID   Q7M390_BALAC PRELIMINARY;      PRT;     8 AA.
AC   Q7M390;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Trypsin (EC 3.4.21.4) precursor (Fragment).
OS   Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC   Mysticeti; Balaenopteridae; Balaenoptera.
OX   NCBI_TaxID=9767;
RN   [1]
RP   PROTEIN SEQUENCE.
RA   Bricteux-Gregoire S., Schyns R., Florkin M., Emmens M., Welling G.W.,
RA   Beintema J.J.;
RT   "N-terminal amino acid sequence of trypsinogen from the lesser
RT   rorqual, Balaenoptera acutorostrata (Cetacea). Simultaneous isolation
RT   of trypsinogen, chymotrypsinogen and ribonuclease from pancreas.";
RL   Biochim. Biophys. Acta 386:244-255(1975).
RN   [2]
RP   PROTEIN SEQUENCE.
RX   PubMed=1125273;
RA   Bricteux-Gregoire S., Schyns R., Florkin M., Emmens M., Welling G.W.,
RA   Beintema J.J.;
RT   "N-terminal amino acid sequence of trypsinogen from the lesser
RT   rorqual, Balaenoptera acutorostrata (Cetacea). Simultaneous isolation
RT   of trypsinogen, chymotrypsinogen and ribonuclease from pancreas.";
RL   Biochim. Biophys. Acta 386:244-255(1975).
DR   PIR; A61328; A61328.
DR   GO; GO:0004295; F:trypsin activity; IEA.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  964 MW;  8D3AAAAAAAA04769 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDD 5
              : ||
Db          3 IDDD 6


RESULT 13
Q8H9K1_9CAUD
ID   Q8H9K1_9CAUD PRELIMINARY;      PRT;     8 AA.
AC   Q8H9K1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Gp30.2 protein (Fragment).
GN   Name=30.2;
OS   Bacteriophage LZ10.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC   T4-like viruses.
OX   NCBI_TaxID=192973;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kolesinskiene G., Nivinskas R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ458400; CAD30256.1; -; Genomic_DNA.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  918 MW;  F3B1A72041B76336 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXD 4
              :| |
Db          5 ILTD 8


RESULT 14
Q8SBJ0_BPR69
ID   Q8SBJ0_BPR69 PRELIMINARY;      PRT;     8 AA.
AC   Q8SBJ0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Gp30.2 (Fragment).
GN   Name=30.2;
OS   Bacteriophage RB69.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC   T4-like viruses.
OX   NCBI_TaxID=12353;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Piesiniene L., Kolesinskiene G., Truncaite L., Zajanckauskaite A.,
RA   Nivinskas R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ439452; CAD28423.1; -; Genomic_DNA.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  918 MW;  F3B1A72041B76336 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXD 4
              :| |
Db          5 ILTD 8


RESULT 15
Q6JC68_SOYBN
ID   Q6JC68_SOYBN PRELIMINARY;      PRT;     8 AA.
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AC   Q6JC68;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Isoflavone synthase 1 (Fragment).
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15356384; DOI=10.1023/B:PLAN.0000040814.28507.35;
RA   Subramanian S., Hu X., Lu G., Odell J.T., Yu O.;
RT   "The promoters of two isoflavone synthase genes respond differentially
RT   to nodulation and defense signals in transgenic soybean roots.";
RL   Plant Mol. Biol. 54:623-639(2004).
DR   EMBL; AY530096; AAT01227.1; -; Genomic_DNA.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  859 MW;  F1772DD72B172726 CRC64;

  Query Match             35.1%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 LLE 8
              |||
Db          2 LLE 4


Search completed: April  6, 2006, 16:25:08
Job time : 120 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:25:31 ; Search time 27.3333 Seconds
(without alignments)
27.222 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	2	US-09-269-250E-18	Sequence 18, Appl
2	36	97.3	9	2	US-09-269-250E-20	Sequence 20, Appl
3	36	97.3	9	2	US-09-269-250E-29	Sequence 29, Appl
4	36	97.3	9	2	US-09-489-760-1	Sequence 1, Appli
5	36	97.3	9	2	US-09-489-760-2	Sequence 2, Appli
6	36	97.3	9	2	US-09-489-760-5	Sequence 5, Appli
7	23	62.2	8	2	US-09-269-250E-38	Sequence 38, Appl
8	22	59.5	7	2	US-08-556-419-14	Sequence 14, Appl
9	22	59.5	9	2	US-09-744-549-15	Sequence 15, Appl
10	22	59.5	9	2	US-10-394-980-421	Sequence 421, App
11	22	59.5	9	2	US-10-394-980-464	Sequence 464, App
12	21	56.8	6	1	US-08-459-568-20	Sequence 20, Appl
13	21	56.8	6	1	US-08-399-411-20	Sequence 20, Appl
14	21	56.8	6	2	US-08-516-859A-20	Sequence 20, Appl
15	21	56.8	6	2	US-09-586-472-20	Sequence 20, Appl
16	21	56.8	6	2	US-09-528-706-20	Sequence 20, Appl
17	21	56.8	8	1	US-08-459-568-75	Sequence 75, Appl
18	21	56.8	8	1	US-08-399-411-75	Sequence 75, Appl
19	21	56.8	8	2	US-08-516-859A-75	Sequence 75, Appl
20	21	56.8	8	2	US-09-586-472-75	Sequence 75, Appl
21	21	56.8	8	2	US-09-528-706-75	Sequence 75, Appl
22	21	56.8	9	1	US-08-459-568-72	Sequence 72, Appl
23	21	56.8	9	1	US-08-459-568-78	Sequence 78, Appl
24	21	56.8	9	1	US-08-399-411-72	Sequence 72, Appl
25	21	56.8	9	1	US-08-399-411-78	Sequence 78, Appl
26	21	56.8	9	2	US-08-516-859A-72	Sequence 72, Appl
27	21	56.8	9	2	US-08-516-859A-78	Sequence 78, Appl
28	21	56.8	9	2	US-09-217-609A-11	Sequence 11, Appl
29	21	56.8	9	2	US-08-873-235B-11	Sequence 11, Appl
30	21	56.8	9	2	US-09-586-472-72	Sequence 72, Appl
31	21	56.8	9	2	US-09-586-472-78	Sequence 78, Appl
32	21	56.8	9	2	US-09-528-706-72	Sequence 72, Appl
33	21	56.8	9	2	US-09-528-706-78	Sequence 78, Appl
34	21	56.8	9	2	US-09-489-760-4	Sequence 4, Appli
35	20	54.1	6	2	US-09-025-819-11	Sequence 11, Appl
36	20	54.1	6	2	US-09-808-126-11	Sequence 11, Appl
37	20	54.1	6	2	US-09-803-951-11	Sequence 11, Appl
38	20	54.1	8	2	US-08-747-599A-47	Sequence 47, Appl
39	20	54.1	8	2	US-08-747-599A-50	Sequence 50, Appl
40	20	54.1	8	2	US-08-747-599A-51	Sequence 51, Appl
41	19	51.4	6	2	US-08-974-549A-373	Sequence 373, App
42	19	51.4	6	2	US-08-912-951-140	Sequence 140, App
43	19	51.4	6	2	US-09-402-181B-373	Sequence 373, App
44	19	51.4	6	2	US-09-721-456-373	Sequence 373, App
45	19	51.4	7	2	US-09-187-859-1186	Sequence 1186, Ap

ALIGNMENTS

RESULT 1
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 97.3%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 97.3%; Score 36; DB 2; Length 9;

```
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 3
US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 4
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
;   OTHER INFORMATION: RESIDUE
US-09-489-760-1

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 5
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Histocompatibility antigen
US-09-489-760-2

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 6
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

  Query Match             97.3%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
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; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN
US-09-269-250E-38

Query Match 62.2%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLLEA 9
||||
Db 4 DLLEA 8

RESULT 8
US-08-556-419-14
; Sequence 14, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-08-556-419-14

Query Match 59.5%; Score 22; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
||||:
Db 1 DDLLQ 5

RESULT 9
US-09-744-549-15
; Sequence 15, Application US/09744549
; Patent No. 6664232
; GENERAL INFORMATION:
; APPLICANT: Itoh, Kyogo et al.
; TITLE OF INVENTION: HLA-A2-restricted Tumor Antigen Peptides Derived From SART-1
; FILE REFERENCE: 0020-4808P
; CURRENT APPLICATION NUMBER: US/09/744,549
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: JP H10-212940
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-744-549-15

Query Match 59.5%; Score 22; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VLXDDLL 7
| ||||
Db 3 VRADDLL 9

RESULT 10
US-10-394-980-421
; Sequence 421, Application US/10394980
; Patent No. 6908740
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 421
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: FR10 - 1624,68
US-10-394-980-421

Query Match 59.5%; Score 22; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LXDDLLE 8
| ||| |
Db 3 LLDDLSE 9

RESULT 11
US-10-394-980-464
; Sequence 464, Application US/10394980
; Patent No. 6908740
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 464

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;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: Table XIX - 1624.68
US-10-394-980-464

  Query Match             59.5%;  Score 22;  DB 2;  Length 9;
  Best Local Similarity   71.4%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LXDDLLE 8
              | |||  |
Db          3 LLDDLSE 9


RESULT 12
US-08-459-568-20
; Sequence 20, Application US/08459568
; Patent No. 5811304
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,568
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-459-568-20

  Query Match             56.8%;  Score 21;  DB 1;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5


RESULT 13
US-08-399-411-20
; Sequence 20, Application US/08399411
; Patent No. 5831008
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/399,411
;      FILING DATE:  06-MAR-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-399-411-20

  Query Match             56.8%;  Score 21;  DB 1;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5


RESULT 14
US-08-516-859A-20
; Sequence 20, Application US/08516859A
; Patent No. 6069231
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/516,859A
;      FILING DATE:  18-AUG-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/292,683
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;      FILING DATE:  18-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1776
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-516-859A-20

  Query Match             56.8%;  Score 21;  DB 2;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5


RESULT 15
US-09-586-472-20
; Sequence 20, Application US/09586472
; Patent No. 6323335
;   GENERAL INFORMATION:
;        APPLICANT: Huang, Shi
;        TITLE OF INVENTION: Retinoblastoma Protein - Interacting
;                            Zinc Finger Proteins
;        NUMBER OF SEQUENCES: 106
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Campbell & Flores LLP
;             STREET: 4370 La Jolla Village Drive, Suite 700
;             CITY: San Diego
;             STATE: California
;             COUNTRY: USA
;             ZIP: 92122
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/586,472
;             FILING DATE: 01-Jun-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/528,706
;             FILING DATE: 17-MAR-2000
;             APPLICATION NUMBER: US 08/516,859
;             FILING DATE: 18-AUG-1995
;             APPLICATION NUMBER: US 08/399,411
;             FILING DATE: 06-MAR-1995
;             APPLICATION NUMBER: US 08/292,683
;             FILING DATE: 18-AUG-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Campbell, Cathryn A.
;             REGISTRATION NUMBER: 31,815
;             REFERENCE/DOCKET NUMBER: P-LJ 4130
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (619) 535-9001
;             TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-586-472-20

  Query Match             56.8%;  Score 21;  DB 2;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5


Search completed: April  6, 2006, 16:27:37
Job time : 27.6667 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:44:31 ; Search time 90.3333 Seconds
(without alignments)
41.629 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	4	US-10-623-176-1	Sequence 1, Appli
2	36	97.3	9	4	US-10-623-176-2	Sequence 2, Appli
3	36	97.3	9	4	US-10-623-176-10	Sequence 10, Appl
4	36	97.3	9	4	US-10-791-217-1	Sequence 1, Appli
5	36	97.3	9	4	US-10-791-217-2	Sequence 2, Appli
6	36	97.3	9	4	US-10-791-217-5	Sequence 5, Appli
7	36	97.3	9	5	US-10-861-335-1	Sequence 1, Appli
8	36	97.3	9	6	US-11-007-740-18	Sequence 18, Appl
9	36	97.3	9	6	US-11-007-740-20	Sequence 20, Appl
10	36	97.3	9	6	US-11-007-740-29	Sequence 29, Appl
11	32	86.5	9	4	US-10-623-176-41	Sequence 41, Appl
12	32	86.5	9	4	US-10-623-176-42	Sequence 42, Appl
13	32	86.5	9	4	US-10-623-176-45	Sequence 45, Appl
14	32	86.5	9	4	US-10-623-176-46	Sequence 46, Appl
15	29	78.4	9	4	US-10-623-176-47	Sequence 47, Appl
16	29	78.4	9	4	US-10-623-176-48	Sequence 48, Appl
17	27	73.0	9	4	US-10-623-176-23	Sequence 23, Appl
18	27	73.0	9	4	US-10-623-176-40	Sequence 40, Appl
19	23	62.2	8	4	US-10-623-176-15	Sequence 15, Appl
20	23	62.2	8	6	US-11-007-740-38	Sequence 38, Appl
21	23	62.2	9	3	US-09-834-765-132	Sequence 132, App
22	23	62.2	9	3	US-09-834-765-349	Sequence 349, App
23	23	62.2	9	4	US-10-623-176-3	Sequence 3, Appli
24	23	62.2	9	4	US-10-623-176-4	Sequence 4, Appli
25	23	62.2	9	4	US-10-623-176-5	Sequence 5, Appli
26	22	59.5	9	4	US-10-119-536A-109	Sequence 109, App
27	22	59.5	9	4	US-10-394-980-421	Sequence 421, App
28	22	59.5	9	4	US-10-394-980-464	Sequence 464, App
29	22	59.5	9	5	US-10-275-652-50	Sequence 50, Appl
30	22	59.5	9	5	US-10-952-557-421	Sequence 421, App
31	22	59.5	9	5	US-10-952-557-464	Sequence 464, App
32	22	59.5	9	5	US-10-996-306-109	Sequence 109, App
33	21	56.8	9	3	US-09-833-203-54	Sequence 54, Appl
34	21	56.8	9	4	US-10-057-475B-10608	Sequence 10608, A
35	21	56.8	9	4	US-10-057-475B-10813	Sequence 10813, A
36	21	56.8	9	4	US-10-154-884B-10608	Sequence 10608, A
37	21	56.8	9	4	US-10-154-884B-10813	Sequence 10813, A
38	21	56.8	9	4	US-10-623-176-14	Sequence 14, Appl
39	21	56.8	9	4	US-10-791-217-4	Sequence 4, Appli
40	21	56.8	9	4	US-10-809-790-23	Sequence 23, Appl
41	21	56.8	9	5	US-10-999-364-73	Sequence 73, Appl
42	21	56.8	9	6	US-11-007-740-40	Sequence 40, Appl
43	20	54.1	5	4	US-10-166-225A-168	Sequence 168, App
44	20	54.1	5	4	US-10-166-225A-169	Sequence 169, App
45	20	54.1	5	4	US-10-166-225A-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; OTHER INFORMATION: wherein X can be R or H
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-1

Query Match 97.3%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9
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RESULT 2
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.

```
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-2

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 3
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-10

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 4
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 5
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 6
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

  Query Match             97.3%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
;  TITLE OF INVENTION:  of tumors
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

  Query Match             97.3%;  Score 36;  DB 5;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 8
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

  Query Match             97.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 9
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

  Query Match             97.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 10
US-11-007-740-29
; Sequence 29, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
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;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29

  Query Match             97.3%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              |||||||||
Db          1 VLXDDLLEA 9


RESULT 11
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-41

  Query Match             86.5%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              || |||||
Db          2 VLHDDLLE 9


RESULT 12
US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-42

  Query Match             86.5%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              || |||||
Db          2 VLRDDLLE 9


RESULT 13
US-10-623-176-45
; Sequence 45, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-45

  Query Match             86.5%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
               | ||||||
```

```
Db          1 LHDDLLEA 8


RESULT 14
US-10-623-176-46
; Sequence 46, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-46

  Query Match             86.5%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LXDDLLEA 9
              | ||||||
Db          1 LRDDLLEA 8


RESULT 15
US-10-623-176-47
; Sequence 47, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-47

  Query Match             78.4%;  Score 29;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              ||||||
Db          2 DDLLEA 7


Search completed: April  6, 2006, 16:50:29
Job time : 91.3333 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:46:11 ; Search time 12.3333 Seconds
(without alignments)
22.762 Million cell updates/sec

Title: US-10-791-217A-1
Perfect score: 37
Sequence: 1 VLXDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 38721

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	97.3	9	7	US-11-010-748A-11	Sequence 11, Appl
2	36	97.3	9	7	US-11-010-748A-12	Sequence 12, Appl
3	21	56.8	9	6	US-10-927-435-63	Sequence 63, Appl
4	21	56.8	9	6	US-10-927-634-63	Sequence 63, Appl
5	20	54.1	5	7	US-11-129-143-168	Sequence 168, App
6	20	54.1	5	7	US-11-129-143-169	Sequence 169, App
7	20	54.1	5	7	US-11-129-143-170	Sequence 170, App
8	20	54.1	5	7	US-11-129-143-171	Sequence 171, App
9	20	54.1	5	7	US-11-129-143-172	Sequence 172, App
10	20	54.1	5	7	US-11-129-143-173	Sequence 173, App
11	20	54.1	7	6	US-10-982-440-126	Sequence 126, App
12	20	54.1	8	7	US-11-021-305-62	Sequence 62, Appl
13	20	54.1	8	7	US-11-021-305-65	Sequence 65, Appl
14	20	54.1	8	7	US-11-021-305-66	Sequence 66, Appl
15	19	51.4	6	7	US-11-207-078-373	Sequence 373, App
16	19	51.4	7	7	US-11-225-686-2954	Sequence 2954, Ap
17	19	51.4	7	7	US-11-225-686-3877	Sequence 3877, Ap
18	19	51.4	7	7	US-11-225-686-3914	Sequence 3914, Ap
19	19	51.4	7	7	US-11-225-686-3915	Sequence 3915, Ap
20	19	51.4	7	7	US-11-225-686-3916	Sequence 3916, Ap
21	19	51.4	7	7	US-11-225-686-3932	Sequence 3932, Ap
22	19	51.4	7	7	US-11-225-686-3941	Sequence 3941, Ap
23	19	51.4	7	7	US-11-202-009-2954	Sequence 2954, Ap
24	19	51.4	7	7	US-11-202-009-3877	Sequence 3877, Ap
25	19	51.4	7	7	US-11-202-009-3914	Sequence 3914, Ap
26	19	51.4	7	7	US-11-202-009-3915	Sequence 3915, Ap
27	19	51.4	7	7	US-11-202-009-3916	Sequence 3916, Ap
28	19	51.4	7	7	US-11-202-009-3932	Sequence 3932, Ap
29	19	51.4	7	7	US-11-202-009-3941	Sequence 3941, Ap
30	19	51.4	9	6	US-10-073-301A-7	Sequence 7, Appli
31	19	51.4	9	6	US-10-989-767A-39	Sequence 39, Appl
32	19	51.4	9	6	US-10-927-435-62	Sequence 62, Appl
33	19	51.4	9	6	US-10-927-634-62	Sequence 62, Appl
34	19	51.4	9	7	US-11-203-137-7	Sequence 7, Appli
35	18	48.6	7	7	US-11-096-706-88	Sequence 88, Appl
36	18	48.6	8	7	US-11-267-631-42	Sequence 42, Appl
37	18	48.6	9	6	US-10-981-873-24	Sequence 24, Appl
38	18	48.6	9	6	US-10-997-759-29	Sequence 29, Appl
39	18	48.6	9	6	US-10-895-064-1363	Sequence 1363, Ap
40	18	48.6	9	6	US-10-989-767A-219	Sequence 219, App
41	18	48.6	9	6	US-10-989-767A-565	Sequence 565, App
42	18	48.6	9	7	US-11-234-786-338	Sequence 338, App
43	18	48.6	9	7	US-11-129-741-1363	Sequence 1363, Ap
44	17	45.9	6	7	US-11-129-143-163	Sequence 163, App
45	17	45.9	6	7	US-11-129-143-164	Sequence 164, App

ALIGNMENTS

RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-11

Query Match 97.3%; Score 36; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLXDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

```
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
;  FILE REFERENCE: MER-136
;  CURRENT APPLICATION NUMBER: US/11/010,748A
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/EP03/06251
;  PRIOR FILING DATE: 2003-06-13
;  PRIOR APPLICATION NUMBER: EP02013423.5
;  PRIOR FILING DATE: 2002-06-13
;  NUMBER OF SEQ ID NOS: 926
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
;   OTHER INFORMATION: ell epitopes
US-11-010-748A-12

  Query Match             97.3%;  Score 36;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 3
US-10-927-435-63
; Sequence 63, Application US/10927435
; Publication No. US20060045884A1
; GENERAL INFORMATION:
;  APPLICANT: MOLLDREM, JEFFREY
;  TITLE OF INVENTION: VACCINES FOR AUTOIMMUNE AND INFECTIOUS DISEASE
;  FILE REFERENCE: UTSC:788USC2
;  CURRENT APPLICATION NUMBER: US/10/927,435
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/489,238
;  PRIOR FILING DATE: 2003-08-26
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-927-435-63

  Query Match             56.8%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              :| | |||
Db          1 ILLDWLLE 8


RESULT 4
US-10-927-634-63
; Sequence 63, Application US/10927634
; Publication No. US20060045881A1
; GENERAL INFORMATION:
;  APPLICANT: MOLLDREM, JEFFREY
;  TITLE OF INVENTION: ANTI-CANCER VACCINES
;  FILE REFERENCE: UTSC:788USC1
;  CURRENT APPLICATION NUMBER: US/10/927,634
;  CURRENT FILING DATE:  2004-08-26
;  PRIOR APPLICATION NUMBER: 60/489,238
;  PRIOR FILING DATE: 2003-08-26
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-927-634-63

  Query Match             56.8%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+05;
  Matches    5;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLXDDLLE 8
              :| | |||
Db          1 ILLDWLLE 8


RESULT 5
US-11-129-143-168
; Sequence 168, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bradyrhizobium japonicum
US-11-129-143-168

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 6
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
;   LENGTH: 5
;   TYPE: PRT
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;   ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-169

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 7
US-11-129-143-170
; Sequence 170, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bacillus stearothermophilus
US-11-129-143-170

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 8
US-11-129-143-171
; Sequence 171, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bacillus subtilis
US-11-129-143-171

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 9
US-11-129-143-172
; Sequence 172, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-11-129-143-172

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 10
US-11-129-143-173
; Sequence 173, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
US-11-129-143-173

  Query Match             54.1%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 11
US-10-982-440-126
; Sequence 126, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
;  APPLICANT: Oliner, John
```

```
;  APPLICANT:  Graham, Kevin
;  TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
;  FILE REFERENCE: 04-881-A
;  CURRENT APPLICATION NUMBER: US/10/982,440
;  CURRENT FILING DATE:  2004-11-04
;  PRIOR APPLICATION NUMBER: 60/620,161
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-440-126

  Query Match             54.1%;  Score 20;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              ||||
Db          2 DDLL 5


RESULT 12
US-11-021-305-62
; Sequence 62, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
;  APPLICANT: Prins, Johannes B
;  APPLICANT:  Hutley, Louise J
;  TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
;  FILE REFERENCE: DAVI169.001CP1
;  CURRENT APPLICATION NUMBER: US/11/021,305
;  CURRENT FILING DATE:  2004-12-23
;  PRIOR APPLICATION NUMBER: USSN 60/392,130
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: mammalian
US-11-021-305-62

  Query Match             54.1%;  Score 20;  DB 7;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              ||||
Db          4 DDLL 7


RESULT 13
US-11-021-305-65
; Sequence 65, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
;  APPLICANT: Prins, Johannes B
;  APPLICANT:  Hutley, Louise J
;  TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
;  FILE REFERENCE: DAVI169.001CP1
;  CURRENT APPLICATION NUMBER: US/11/021,305
;  CURRENT FILING DATE:  2004-12-23
;  PRIOR APPLICATION NUMBER: USSN 60/392,130
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: mammalian
US-11-021-305-65

  Query Match             54.1%;  Score 20;  DB 7;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              ||||
Db          4 DDLL 7


RESULT 14
US-11-021-305-66
; Sequence 66, Application US/11021305
; Publication No. US20050282733A1
; GENERAL INFORMATION:
;  APPLICANT: Prins, Johannes B
;  APPLICANT:  Hutley, Louise J
;  TITLE OF INVENTION: Differentiation-modulating agents and uses therefor
;  FILE REFERENCE: DAVI169.001CP1
;  CURRENT APPLICATION NUMBER: US/11/021,305
;  CURRENT FILING DATE:  2004-12-23
;  PRIOR APPLICATION NUMBER: USSN 60/392,130
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 170
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: mammalian
US-11-021-305-66

  Query Match             54.1%;  Score 20;  DB 7;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLL 7
              ||||
Db          4 DDLL 7


RESULT 15
US-11-207-078-373
; Sequence 373, Application US/11207078
; Publication No. US20060040307A1
;   GENERAL INFORMATION:
;        APPLICANT: Cech, Thomas R.
;                   Lingner, Joachim
;                   Nakamura, Toru
;                   Chapman, Karen B.
;                   Morin, Gregg B.
;                   Harley, Calvin B.
;                   Andrews, William H.
;        TITLE OF INVENTION: Human Telomerase Catalytic Subunit
;        NUMBER OF SEQUENCES: 727
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/207,078
;             FILING DATE: 17-Aug-2005
;             CLASSIFICATION: <Unknown
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/721,477
```

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;              FILING DATE: 22-Nov-2000
;              APPLICATION NUMBER: 08/974,549
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: US 08/844,419
;              FILING DATE: 18-APR-1997
;              APPLICATION NUMBER: US 08/846,017
;              FILING DATE: 25-APR-1997
;              APPLICATION NUMBER: US 08/851,843
;              FILING DATE: 06-MAY-1997
;              APPLICATION NUMBER: US 08/854,050
;              FILING DATE: 09-MAY-1997
;              APPLICATION NUMBER: US 08/911,312
;              FILING DATE: 14-AUG-1997
;              APPLICATION NUMBER: US 08/912,951
;              FILING DATE: 14-AUG-1997
;              APPLICATION NUMBER: US 08/915,503
;              FILING DATE: 14-AUG-1997
;              APPLICATION NUMBER: WO PCT/US97/17618
;              FILING DATE: 01-OCT-1997
;              APPLICATION NUMBER: WO PCT/US97/17885
;              FILING DATE: 01-OCT-1997
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Apple, Randolph Ted
;              REGISTRATION NUMBER: 36,429
;              REFERENCE/DOCKET NUMBER: 015389-002610US
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (415) 576-0200
;              TELEFAX: (415) 576-0300
;    INFORMATION FOR SEQ ID NO: 373:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 6 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         SEQUENCE DESCRIPTION: SEQ ID NO: 373:
US-11-207-078-373

  Query Match             51.4%;  Score 19;  DB 7;  Length 6;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LXDDLL 7
              | || |
Db          1 LVDDFL 6


Search completed: April  6, 2006, 16:51:12
Job time : 13.3333 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:12:46 ; Search time 111.667 Seconds
(without alignments)
35.413 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	2	AAW99196	Aaw99196 Minor his
2	45	100.0	9	2	AAW97375	Aaw97375 HA-1 H-al
3	45	100.0	9	8	ADH40333	Adh40333 Human min
4	37	82.2	9	2	AAW99197	Aaw99197 Minor his
5	37	82.2	9	2	AAW97374	Aaw97374 HA-1 R-al
6	37	82.2	9	8	ADH40334	Adh40334 Human min
7	36	80.0	9	2	AAW99195	Aaw99195 Minor his
8	36	80.0	9	2	AAW97572	Aaw97572 T-cell ep
9	31	68.9	9	8	ADU99853	Adu99853 BCZ4 tumo
10	30	66.7	9	2	AAW97373	Aaw97373 Peptide e
11	28	62.2	9	2	AAY10122	Aay10122 T cell ep
12	28	62.2	9	5	ABG79805	Abg79805 MHC class
13	28	62.2	9	8	ADK68732	Adk68732 Epitope 1
14	28	62.2	9	8	ADK05291	Adk05291 Hepatitis
15	28	62.2	9	8	ADK05293	Adk05293 Hepatitis
16	28	62.2	9	8	ADQ10530	Adq10530 Cercopith
17	28	62.2	9	8	ADS81010	Ads81010 Tumour-as
18	27	60.0	9	6	ABJ20115	Abj20115 MHC bindi
19	27	60.0	9	8	ADT02787	Adt02787 Human tum
20	26	57.8	6	6	ABU97233	Abu97233 Enzyme pe
21	26	57.8	6	6	ABU97232	Abu97232 Enzyme pe
22	26	57.8	6	6	ABU97234	Abu97234 Enzyme pe
23	26	57.8	6	6	ABU97231	Abu97231 Enzyme pe
24	26	57.8	6	9	ADY63770	Ady63770 Human alb
25	26	57.8	7	8	ADM96262	Adm96262 Human ser
26	26	57.8	9	5	AAE31275	Aae31275 Human mag
27	26	57.8	9	8	ADM96261	Adm96261 Human ser
28	26	57.8	9	8	ADM96258	Adm96258 Human ser
29	26	57.8	9	8	ADT73023	Adt73023 Human RSV
30	26	57.8	9	8	ADT49074	Adt49074 Human BFA
31	26	57.8	9	8	ADU99636	Adu99636 BFA5 tumo
32	25	55.6	6	6	ABU97229	Abu97229 Enzyme pe
33	25	55.6	6	6	ABU97230	Abu97230 Enzyme pe
34	25	55.6	9	4	AAG79144	Aag79144 Amino ter
35	25	55.6	9	4	AAB84492	Aab84492 Peptide f
36	25	55.6	9	5	AAE26631	Aae26631 Yeast GPA
37	25	55.6	9	7	ADC25889	Adc25889 Yeast GPA
38	24	53.3	6	2	AAR29358	Aar29358 Endotheli
39	24	53.3	6	2	AAR69140	Aar69140 Endotheli
40	24	53.3	7	2	AAW33386	Aaw33386 Altered I
41	24	53.3	7	4	AAB70589	Aab70589 Human imm
42	24	53.3	7	5	AAO21066	Aao21066 Isomerise
43	24	53.3	7	5	AAE28095	Aae28095 Human imm
44	24	53.3	8	8	ADT39474	Adt39474 hSARS vir
45	24	53.3	8	8	ADS78893	Ads78893 SARS viru

ALIGNMENTS

RESULT 1
AAW99196
ID AAW99196 standard; peptide; 9 AA.
XX
AC AAW99196;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

```
  Query Match             100.0%;  Score 45;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 2
AAW97375
ID   AAW97375 standard; protein; 9 AA.
XX
AC   AAW97375;
XX
DT   13-MAY-1999  (first entry)
XX
DE   HA-1 H-allele sequence.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Claim 18; Fig 5; 59pp; English.
XX
CC   The present sequence represents part of the minor histocompatibility
CC   antigen HA-1 H-allele. The specification describes methods for typing
CC   alleles (preferably the H and R alleles) of the minor histocompatibility
CC   antigen HA-1 in a sample, which comprise detecting polymorphic
CC   nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC   methods can be used for HA-1 typing for bone marrow transplants, severe
CC   aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC   detection of genetic aberrances. The probes and primers of the invention
CC   can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC   anti-idiotypic B cells and/or T cells and antibodies
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 3
ADH40333
ID   ADH40333 standard; peptide; 9 AA.
XX
AC   ADH40333;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW   human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW   minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS   Homo sapiens.
XX
PN   WO2003106692-A2.
XX
PD   24-DEC-2003.
XX
PF   13-JUN-2003; 2003WO-EP006251.
XX
PR   13-JUN-2002; 2002EP-00013423.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Strittmatter W,  Moll H;
XX
DR   WPI; 2004-082200/08.
XX
PT   Providing allelic variant epitope of protein based on single nucleotide
PT   polymorphism by defining target protein, screening database of protein,
PT   identifying, selecting allelic variant protein, creating variant
PT   epitopes.
XX
PS   Disclosure; Page 82; 119pp; English.
XX
CC   The invention relates to a novel method for providing epitopes of allelic
CC   variants of antigenic proteins from specific species based on single
CC   nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC   subset, screening database of DNA encoding target protein, identifying,
CC   selecting allelic peptide/protein variants, expression product or its
CC   fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC   selecting epitopes binding to MHC protein. A protein of the invention has
CC   cytostatic activity, and may have a use in a vaccine. The method is
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             100.0%;  Score 45;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 4
AAW99197
ID   AAW99197 standard; peptide; 9 AA.
XX
AC   AAW99197;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
```

XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 5
AAW97374
ID AAW97374 standard; protein; 9 AA.
XX
AC AAW97374;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 R-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 13; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 R-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC anti-idiotypic B cells and/or T cells and antibodies
XX
SQ Sequence 9 AA;

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 6
ADH40334
ID ADH40334 standard; peptide; 9 AA.
XX
AC ADH40334;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS Homo sapiens.
XX
PN WO2003106692-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-EP006251.
XX
PR 13-JUN-2002; 2002EP-00013423.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Strittmatter W, Moll H;
XX
DR WPI; 2004-082200/08.
XX
PT Providing allelic variant epitope of protein based on single nucleotide
PT polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.
XX
PS Disclosure; Page 82; 119pp; English.
XX
CC The invention relates to a novel method for providing epitopes of allelic
CC variants of antigenic proteins from specific species based on single
CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC subset, screening database of DNA encoding target protein, identifying,
CC selecting allelic peptide/protein variants, expression product or its
CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC selecting epitopes binding to MHC protein. A protein of the invention has
CC cytostatic activity, and may have a use in a vaccine. The method is

```
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             82.2%;  Score 37;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 7
AAW99195
ID   AAW99195 standard; peptide; 9 AA.
XX
AC   AAW99195;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /label= His, Arg
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             80.0%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 8
AAW97572
ID   AAW97572 standard; peptide; 9 AA.
XX
AC   AAW97572;
XX
DT   20-MAY-1999  (first entry)
XX
DE   T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW   T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW   transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW   neoplastic haematopoietic cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /note= "His or Arg"
XX
PN   WO9905173-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000424.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-142855/12.
XX
PT   Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT   for inducing tolerance to transplants and prevent rejection or graft-
PT   versus-host disease.
XX
PS   Claim 1; Page 39; 57pp; English.
XX
CC   The present sequence represents an immunogenic peptide constituting a T-
CC   cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC   The peptide can be used in vaccines or pharmaceutical formulations as
CC   medicines to induce tolerance for transplants so as to prevent rejection
CC   and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC   Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC   I context, can be eliminated after specific recognition of the peptides.
CC   The peptides can also be used to raise antibodies, T-cell receptor, B-
CC   and T-cells
XX
SQ   Sequence 9 AA;

  Query Match             80.0%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 9
ADU99853
ID   ADU99853 standard; peptide; 9 AA.
```

```
XX
AC   ADU99853;
XX
DT   24-FEB-2005  (first entry)
XX
DE   BCZ4 tumor antigen antigenic peptide #85.
XX
KW   expression vector; tumor antigen; cancer; cytostatic; BCZ4;
KW   antigenic peptide.
XX
OS   Unidentified.
XX
PN   WO2004104039-A2.
XX
PD   02-DEC-2004.
XX
PF   15-MAY-2004; 2004WO-US015202.
XX
PR   16-MAY-2003; 2003US-0471119P.
PR   16-MAY-2003; 2003US-0471193P.
XX
PA   (AVET ) AVENTIS PASTEUR INC.
XX
PI   Berinstein N,  Gallichan S,  Lovitt C,  Parrington M,  Radvanyi L;
PI   Singh-Sandhu D;
XX
DR   WPI; 2004-834272/82.
XX
PT   New expression vector comprising a nucleic acid encoding a tumor antigen,
PT   e.g. BFA4, BCY1, BFA5, BCZ4, or BFY3, useful for expressing multiple
PT   tumor antigens, or for preventing or treating cancer.
XX
PS   Example 8; Page 60; 109pp; English.
XX
CC   The invention comprises an expression vector that contains a nucleic acid
CC   encoding a tumor antigen (e.g. BCZ4 or BFY3). The expression vector of
CC   the invention is useful for the expression of multiple tumor antigens and
CC   the prevention or treatment of cancer. The present amino acid sequence
CC   represents a BCZ4 tumor antigen antigenic peptide that was used in an
CC   example of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             68.9%;  Score 31;  DB 8;  Length 9;
  Best Local Similarity   85.7%;  Pred. No. 2e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              || ||||
Db          2 LHSDLLE 8


RESULT 10
AAW97373
ID   AAW97373 standard; peptide; 9 AA.
XX
AC   AAW97373;
XX
DT   13-MAY-1999  (first entry)
XX
DE   Peptide epitope of HA-1 antigen.
XX
KW   Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW   R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW   severe aplastic anaemia; leukaemia; immune deficiency disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2
FT                   /note= "not specified"
FT   Misc-difference 6
FT                   /note= "not specified"
FT   Misc-difference 7
FT                   /note= "not specified"
XX
PN   WO9905313-A2.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-EP004928.
XX
PR   23-JUL-1997;   97EP-00202303.
PR   02-JUN-1998;   98EP-00870125.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy E;
XX
DR   WPI; 1999-142960/12.
XX
PT   Typing minor histocompatibility antigen HA-1 - by amplifying and
PT   identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT   of genetic aberrances.
XX
PS   Example 1; Page 22; 59pp; English.
XX
CC   The present sequence represents an epitope of the minor
CC   histocompatibility antigen HA-1. The specification describes methods for
CC   typing alleles (preferably the H and R alleles) of the minor
CC   histocompatibility antigen HA-1 in a sample, which comprise detecting
CC   polymorphic nucleotides in the cDNA or genomic nucleic acids of the
CC   alleles. The methods can be used for HA-1 typing for bone marrow
CC   transplants, severe aplastic anaemia, leukaemia and immune deficiency
CC   diseases, as well as detection of genetic aberrances. The probes and
CC   primers of the invention can be used to screen for the HA-1 alleles. The
CC   HA-1 peptides can be used anti-idiotypic B cells and/or T cells and
CC   antibodies
XX
SQ   Sequence 9 AA;

  Query Match             66.7%;  Score 30;  DB 2;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2e+06;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              | |||  ||
Db          1 VXHDDXXEA 9


RESULT 11
AAY10122
ID   AAY10122 standard; peptide; 9 AA.
XX
AC   AAY10122;
XX
DT   12-MAY-1999  (first entry)
XX
DE   T cell epitope/MHC ligand SEQ ID NO:52.
XX
KW   Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
KW   immunisation; tumour; infectious disease; immunotherapy; cancer;
KW   malignant melanoma; viral disease; hepatitis; AIDS.
XX
OS   Synthetic.
OS   Human herpesvirus 4.
XX
PN   WO9902183-A2.
XX
PD   21-JAN-1999.
XX
PF   10-JUL-1998;   98WO-US014289.
XX
PR   10-JUL-1997;   97CA-02209815.
PR   10-DEC-1997;   97US-00988320.
XX
```

PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI Kuendig TM, Simard JJL;
XX
DR WPI; 1999-120514/10.
XX
PT Inducing a cytotoxic T lymphocyte response - by maintaining a level of
PT antigen in the lymphatic system of a mammal so as to provide a sustained
PT CTL response, used to treat, e.g. AIDS.
XX
PS Disclosure; Page 25; 199pp; English.
XX
CC The present invention describes a method of inducing and/or sustaining an
CC immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
CC method comprises: (a) delivering an antigen to the mammal at a level to
CC induce an immunological CTL response in the mammal; and (b) maintaining
CC the level of the antigen in the mammal's lymphatic system to maintain the
CC immunologic CTL response. The method can be used for the delivery of e.g.
CC a differentiation antigen, a tumour-specific multilineage antigen, an
CC embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene
CC antigen, or a viral antigen. They can be used for the treatment of
CC disease such as cancer, e.g. malignant melanoma or infectious disease,
CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
CC to the lymphatic system provides for potent CTL stimulation that takes
CC place in the milieu of the lymphoid organ, and it sustains stimulation
CC that is necessary to keep CTL active, cytotoxic and recirculating through
CC the body. AAY10071 to AAY10639 represent examples of peptide antigens
CC given in the present invention
XX
SQ Sequence 9 AA;

Query Match 62.2%; Score 28; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDL 6
||| :||
Db 4 VLHEDL 9

RESULT 12
ABG79805
ID ABG79805 standard; peptide; 9 AA.
XX
AC ABG79805;
XX
DT 06-AUG-2003 (revised)
DT 15-NOV-2002 (first entry)
XX
DE MHC class I molecule, viral epitope #53.
XX
KW Major histocompatibility complex; MHC; MHC class I molecule; virus;
KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;
KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;
KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
KW acquired immune deficiency syndrome; AIDS.
XX
OS Cercopithecine herpesvirus 15.
XX
PN WO200262368-A2.
XX
PD 15-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US002033.
XX
PR 02-FEB-2001; 2001US-00776232.
XX
PA (CTLI-) CTL IMMUNOTHERAPIES CORP.
XX
PI Kundig TM, Simard JJL;
XX
DR WPI; 2002-657506/70.
XX
PT Inducing or sustaining immunological cytotoxic T lymphocyte response in a
PT mammal, useful for treating a mammal with malignant tumor or infectious
PT disease, by directly administering an antigen to the lymphatic system of
PT the mammal.
XX
PS Disclosure; Page 19; 73pp; English.
XX
CC The invention relates to a method of inducing and/or sustaining an
CC immunological cytotoxic T lymphocyte (CTL) response in a mammal
CC comprising administering directly to the lymphatic system of the mammal:
CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a
CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
CC method is useful for inducing and/or sustaining CTL response in a mammal.
CC This is particularly useful for treating a mammal having a malignant
CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious
CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
CC malaria, measles or tuberculosis), or in an animal having a
CC predisposition to these diseases. The mammal may be dogs, cats, mice,
CC cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-
CC ABG80319 represent viral epitopes on major histocompatibility complex
CC (MHC) class I molecules, used in the method of the invention. (Updated on
CC 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 9 AA;

Query Match 62.2%; Score 28; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDL 6
||| :||
Db 4 VLHEDL 9

RESULT 13
ADK68732
ID ADK68732 standard; peptide; 9 AA.
XX
AC ADK68732;
XX
DT 06-MAY-2004 (first entry)
XX
DE Epitope liberation-related peptide SeqID95.
XX
KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.
XX
OS Human herpesvirus 4.
XX
PN US2003228634-A1.
XX
PD 11-DEC-2003.
XX
PF 07-NOV-2002; 2002US-00292413.
XX
PR 07-NOV-2001; 2001US-0336968P.
XX
PA (SIMA/) SIMARD J J L.
PA (DIAM/) DIAMOND D C.
PA (QIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX
PI Simard JJL, Diamond DC, Qiu Z, Lei X;
XX
DR WPI; 2004-167209/16.
XX
PT Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT liberation by contacting substrate polypeptide comprising epitope of
PT interest, with proteasome, and assaying for liberation of epitope.
XX
PS Disclosure; SEQ ID NO 95; 67pp; English.

```
XX
CC   This invention relates to a novel method of identifying a polypeptide
CC   suitable for epitope liberation, including the steps of identifying an
CC   epitope of interest; providing substrate polypeptide sequence including
CC   the epitope, wherein the substrate permits processing by a proteasome;
CC   contacting the substrate with a composition including the proteasome,
CC   under conditions that support processing of the substrate by proteasome;
CC   and assaying for liberation of epitope. The invention may be useful for
CC   the development of compounds with a cytostatic, antibacterial,
CC   protozoacide or fungicide activity acting as T-cell activators. In
CC   addition, the invention may allow development of a vaccine. The invention
CC   is useful for identifying a polypeptide suitable for epitope liberation,
CC   where the epitope is a housekeeping epitope. The compositions comprising
CC   the identified housekeeping epitopes are useful in vitro in vaccine
CC   development or in the generation or expansion of cytotoxic T lymphocyte
CC   (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC   for activating T-cells against neoplastic cells, and cells infected with
CC   virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC   on the knowledge that such epitopes are, in fact, produced by the
CC   housekeeping proteasome system. Once identified, these epitopes, embodied
CC   as peptides, can be used to successfully immunise or induce therapeutic
CC   CTL responses against housekeeping proteasome expressing target cells in
CC   the host. The present sequence is that of a peptide which is related to
CC   the method of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             62.2%;  Score 28;  DB 8;  Length 9;
  Best Local Similarity   83.3%;  Pred. No. 2e+06;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              |||:||
Db          4 VLHEDL 9


RESULT 14
ADK05291
ID   ADK05291 standard; peptide; 9 AA.
XX
AC   ADK05291;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Hepatitis C virus CTL epitope peptide #3121.
XX
KW   pathogenic virus; alternative reading frame; antigenic determinant;
KW   virucide; vaccine; therapeutic agent; infection; epitope peptide;
KW   HLA-allele; CTL.
XX
OS   Hepatitis C virus.
XX
PN   WO2004011650-A2.
XX
PD   05-FEB-2004.
XX
PF   24-JUL-2003; 2003WO-EP008112.
XX
PR   24-JUL-2002; 2002AT-00001124.
PR   11-JUL-2003; 2003EP-00450171.
XX
PA   (INTE-) INTERCELL AG.
XX
PI   Mattner F,  Schmidt W,  Habel A;
XX
DR   WPI; 2004-169243/16.
XX
PT   New polypeptide encoded by an alternative reading frame of a pathogenic
PT   virus comprising an antigenic determinant, useful for treating or
PT   preventing an infection with the pathogenic virus.
XX
PS   Claim 14; Page 114; 220pp; English.
XX
CC   This invention relates to a novel polypeptide encoded by an alternative
CC   reading frame of a pathogenic virus, where the polypeptide starts with a
CC   methionine amino acid residue, which comprises an antigenic determinant
CC   and more than 7 amino acid residues. The invention may be useful for the
CC   production of compounds with a virucide activity or the development of a
CC   vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC   agent. It is also useful for the manufacture of a medicament for treating
CC   or preventing an infection with the pathogenic virus. The present
CC   sequence is that of a hepatitis C virus CTL epitope peptide of the
CC   invention.
XX
SQ   Sequence 9 AA;

  Query Match             62.2%;  Score 28;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HDDLL 7
              |||||
Db          4 HDDLL 8


RESULT 15
ADK05293
ID   ADK05293 standard; peptide; 9 AA.
XX
AC   ADK05293;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Hepatitis C virus CTL epitope peptide #3123.
XX
KW   pathogenic virus; alternative reading frame; antigenic determinant;
KW   virucide; vaccine; therapeutic agent; infection; epitope peptide;
KW   HLA-allele; CTL.
XX
OS   Hepatitis C virus.
XX
PN   WO2004011650-A2.
XX
PD   05-FEB-2004.
XX
PF   24-JUL-2003; 2003WO-EP008112.
XX
PR   24-JUL-2002; 2002AT-00001124.
PR   11-JUL-2003; 2003EP-00450171.
XX
PA   (INTE-) INTERCELL AG.
XX
PI   Mattner F,  Schmidt W,  Habel A;
XX
DR   WPI; 2004-169243/16.
XX
PT   New polypeptide encoded by an alternative reading frame of a pathogenic
PT   virus comprising an antigenic determinant, useful for treating or
PT   preventing an infection with the pathogenic virus.
XX
PS   Claim 14; Page 114; 220pp; English.
XX
CC   This invention relates to a novel polypeptide encoded by an alternative
CC   reading frame of a pathogenic virus, where the polypeptide starts with a
CC   methionine amino acid residue, which comprises an antigenic determinant
CC   and more than 7 amino acid residues. The invention may be useful for the
CC   production of compounds with a virucide activity or the development of a
CC   vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC   agent. It is also useful for the manufacture of a medicament for treating
CC   or preventing an infection with the pathogenic virus. The present
CC   sequence is that of a hepatitis C virus CTL epitope peptide of the
CC   invention.
XX
SQ   Sequence 9 AA;

  Query Match             62.2%;  Score 28;  DB 8;  Length 9;
```

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 HDDLL 7
              |||||
Db          4 HDDLL 8
```

Search completed: April 6, 2006, 16:19:13
Job time : 114.667 secs

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:19:36 ; Search time 18.6667 Seconds
(without alignments)
46.390 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	40.0	7	2	I46868	alpha-myosin heavy
2	17	37.8	9	2	S55696	phosphoenolpyruvat
3	16	35.6	7	2	PQ0663	membrane protein -
4	16	35.6	7	2	S68004	hucolin, 75K chain
5	16	35.6	8	2	PC4131	hypothetical prote
6	15	33.3	6	2	S78764	ribosomal protein
7	15	33.3	7	2	A59489	protein kinase C i
8	14	31.1	7	2	S20446	elastase - Pseudom
9	14	31.1	8	2	XGHUEU	urine glycopeptide
10	14	31.1	9	2	A12872	transaldolase (EC
11	14	31.1	9	2	S10920	venom protein HR-3
12	14	31.1	9	2	A60427	macrophage cytotox
13	13	28.9	8	2	A61328	trypsin (EC 3.4.21
14	13	28.9	9	2	PH0942	T-cell receptor be
15	12	26.7	4	2	I40697	biotin A - Citroba
16	12	26.7	5	2	PT0679	T-cell receptor be
17	12	26.7	5	2	PT0601	T-cell receptor be
18	12	26.7	6	2	B35640	cerebellar degener
19	12	26.7	6	2	PT0533	T-cell receptor be
20	12	26.7	7	2	A34026	acetylcholinestera
21	12	26.7	7	2	B39040	calsequestrin, fas
22	12	26.7	7	2	PT0628	T-cell receptor be
23	12	26.7	7	2	PT0722	T-cell receptor be
24	12	26.7	7	2	PT0576	T-cell receptor be
25	12	26.7	8	2	PT0368	Ig gamma chain C r
26	12	26.7	8	2	PN0043	phosphatidylethano
27	12	26.7	8	2	PT0557	T-cell receptor be
28	12	26.7	9	2	A60108	exotoxin A - Strep
29	12	26.7	9	2	PW0002	chlorophyll a/b-bi
30	12	26.7	9	2	S65913	pyrimidine synthes
31	12	26.7	9	2	PH0108	late G1-69 protein
32	12	26.7	9	2	PT0562	T-cell receptor be
33	12	26.7	9	2	B30572	T-cell receptor be
34	11	24.4	5	2	C41225	copper resistance
35	11	24.4	5	2	T10954	hypothetical prote
36	11	24.4	6	2	T11779	phosphoglycerate t
37	11	24.4	7	2	S25266	pilE protein - Esc
38	11	24.4	7	2	PT0246	Ig heavy chain CRD
39	11	24.4	8	2	S22428	chitin-binding pro
40	11	24.4	8	2	B33099	158K exoantigen -
41	11	24.4	8	2	S69165	ferredoxin a2 - Ja
42	11	24.4	9	2	S66419	tetrameric protein
43	11	24.4	9	2	PT0272	Ig heavy chain CRD
44	11	24.4	9	2	A11497	transaldolase (EC
45	11	24.4	9	2	B39504	octamer-binding pr

ALIGNMENTS

RESULT 1
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricul
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: UNIPROT:Q28742; UNIPARC:UPI0000087938; GB:K01698; NID:g165538; PIDN

Query Match 40.0%; Score 18; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 LHDD 5
              :||:
Db          3 MHDE 6
```

RESULT 2
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55696
R;Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Tr
A;Reference number: S55696; MUID:95284106; PMID:7766679
A;Accession: S55696
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <HUN>
A;Cross-references: UNIPROT:Q7M3S5; UNIPARC:UPI000017B599

Query Match 37.8%; Score 17; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLHDDL 6
              ::| :|
Db          3 IIHKNL 8
```

RESULT 3
PQ0663

membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C;Species: porcine epidemic diarrhea virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C;Accession: PQ0663
R;Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic
issible gastroenteritis virus.
A;Reference number: JQ2191; MUID:93389433; PMID:8397280
A;Accession: PQ0663
A;Molecule type: mRNA
A;Residues: 1-7 <BRI>
A;Cross-references: UNIPARC:UPI0000170FAC; GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:
C;Comment: This virus is coronavirus related to human coronavirus 229E.
C;Keywords: membrane protein

Query Match 35.6%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLH 3
||| |
Db 3 VLH 5

RESULT 4
S68004
hucolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>
A;Cross-references: UNIPARC:UPI000017C164

Query Match 35.6%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
||| |
Db 4 DDL 6

RESULT 5
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: PC4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding
y for biosynthesis of heme d1.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
A;Accession: PC4131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <KAW>
A;Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:g1217594
A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
C;Superfamily: Pseudomonas stutzeri nirD protein

Query Match 35.6%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
||| |
Db 2 DDL 4

RESULT 6
S78764
ribosomal protein MRP-S23, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78764
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78764
A;Molecule type: protein
A;Residues: 1-6 <GRA>
A;Cross-references: UNIPARC:UPI000017C570
C;Keywords: mitochondrion
F;1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>

Query Match 33.3%; Score 15; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LHDD 5
|| | |
Db 1 LHVD 4

RESULT 7
A59489
protein kinase C inhibitor - rat (fragment)
C;Species: Rattus norvegicus
C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C;Accession: A59489
R;Negoro, M.
submitted to the Protein Sequence Database, June 2003
A;Description: Purification of PKCI from rat liver.
A;Reference number: A59489
A;Accession: A59489
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NEG>
A;Experimental source: strain Wistar, liver
A;Note: p-Hydroxyacetophenone-Sepharose binding protein

Query Match 33.3%; Score 15; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VLHDD 5
: ||
Db 2 IFEDD 6

RESULT 8
S20446
elastase - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C;Accession: S20446
R;Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291-293, 1992
A;Title: Identification of cleavage sites involved in proteolytic processing of Pseudom
A;Reference number: S20446; MUID:92183956; PMID:1544509
A;Accession: S20446
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <KES>
A;Cross-references: UNIPARC:UPI000017A95F

Query Match 31.1%; Score 14; DB 2; Length 7;

```
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              ||::
Db          3 DLID 6


RESULT 9
XGHUEU
urine glycopeptide - human
C;Species: Homo sapiens (man)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C;Accession: A03188
R;Lote, C.J.; Weiss, J.B.
Biochem. J. 123, 25P, 1971
A;Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
A;Reference number: A03188; MUID:72062338; PMID:5126885
A;Accession: A03188
A;Molecule type: protein
A;Residues: 1-8 <LOT>
A;Cross-references: UNIPROT:P02729; UNIPARC:UPI000012B849
C;Comment: The identity of the glycoprotein from which this peptide is derived is unknow
re has also been found (see PIR:XGHUE).
C;Keywords: glycoprotein
F;1/Binding site: carbohydrate (Cys) (covalent) #status experimental

  Query Match             31.1%;  Score 14;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HD 4
              ||
Db          5 HD 6


RESULT 10
A12872
transaldolase (EC 2.2.1.2) I - yeast (Pichia jadinii) (fragment)
C;Species: Pichia jadinii, Candida utilis
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A12872
R;Sun, S.C.; Joris, L.; Tsolas, O.
Arch. Biochem. Biophys. 178, 69-78, 1977
A;Title: Purification and crystallization of transaldolase isozyme I and evidence for di
A;Reference number: A12872; MUID:77110646; PMID:556924
A;Accession: A12872
A;Molecule type: protein
A;Residues: 1-9 <SUN>
A;Cross-references: UNIPROT:P17440; UNIPARC:UPI0000136884
C;Keywords: transferase

  Query Match             31.1%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LHDDLL 7
              :| : |
Db          3 IHCBTL 8


RESULT 11
S10920
venom protein HR-3 - oriental hornet (fragment)
C;Species: Vespa orientalis (oriental hornet)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S10920
R;Tuichibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. St
A;Reference number: S06445
A;Accession: S10920
A;Molecule type: protein
A;Residues: 1-9 <TUI>
A;Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07
C;Keywords: venom

  Query Match             31.1%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   28.6%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              :|: |::
Db          3 VHEFLVK 9


RESULT 12
A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60427
R;Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-induci
A;Reference number: A60427; MUID:91372335; PMID:1909970
A;Accession: A60427
A;Molecule type: protein
A;Residues: 1-9 <JON>
A;Cross-references: UNIPROT:Q7M4R5; UNIPARC:UPI0000142BE0
A;Note: the sequence from the text on page 706 is inconsistent with that from page 708
C;Keywords: cytokine

  Query Match             31.1%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHD 4
              || |
Db          4 VLED 7


RESULT 13
A61328
trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C;Accession: A61328
R;Bricteux-Gregoire, S.; Schyns, R.; Florkin, M.; Emmens, M.; Welling, G.W.; Beintema,
Biochim. Biophys. Acta 386, 244-255, 1975
A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaeno
creas.
A;Reference number: A61328; MUID:75146765; PMID:1125273
A;Accession: A61328
A;Molecule type: protein
A;Residues: 1-8 <BRI>
A;Cross-references: UNIPROT:Q7M390; UNIPARC:UPI000017C43F
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-8/Domain: activation peptide #status experimental <APT>

  Query Match             28.9%;  Score 13;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LHDD 5
              : ||
Db          3 IDDD 6


RESULT 14
PH0942
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0942
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
```

J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0942
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Cross-references: UNIPARC:UPI000017C9DD
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon TGC for residue 2 as Ala
C;Keywords: T-cell receptor

Query Match 28.9%; Score 13; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LLE 8
||||
Db 5 LLE 7

RESULT 15
I40697
biotin A - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40697
R;Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A;Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacte
A;Reference number: I40697; MUID:89006280; PMID:2971595
A;Accession: I40697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: UNIPROT:P13071; UNIPARC:UPI000017AA21; GB:M21922; NID:g144434

Query Match 26.7%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 3 DD 4

Search completed: April 6, 2006, 16:26:11
Job time : 19.6667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:13:46 ; Search time 118 Seconds
(without alignments)
53.811 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	42.2	9	2	Q7R8X5_PLAYO	Q7r8x5 plasmodium
2	19	42.2	9	2	Q47556_ECOLI	Q47556 escherichia
3	18	40.0	7	2	Q28742_RABIT	Q28742 oryctolagus
4	17	37.8	9	2	Q7M3S5_9TRYP	Q7m3s5 trypanosoma
5	16	35.6	7	2	O99182_9SMEG	O99182 gnatholebia
6	16	35.6	8	2	Q7Z6G0_HUMAN	Q7z6g0 homo sapien
7	16	35.6	9	1	FAR8_MACRS	P83281 macrobrachi
8	16	35.6	9	2	Q70SM2_HUMAN	Q70sm2 homo sapien
9	16	35.6	9	2	Q4X981_PLACH	Q4x981 plasmodium
10	16	35.6	9	2	Q8LPT5_MAIZE	Q8lpt5 zea mays (m
11	16	35.6	9	2	P82568_STRPY	P82568 streptococc
12	15	33.3	8	2	Q15900_HUMAN	Q15900 homo sapien
13	15	33.3	8	2	Q4XT27_PLACH	Q4xt27 plasmodium
14	15	33.3	9	2	Q9XJN0_9VIRU	Q9xjn0 bacteriopha
15	14	31.1	6	1	TRPI_PSEPU	P36414 pseudomonas
16	14	31.1	8	1	GLUR_HUMAN	P02729 homo sapien
17	14	31.1	8	2	Q9BFA7_MACPR	Q9bfa7 macroscelid
18	14	31.1	8	2	P72279_RHOGO	P72279 rhodococcus
19	14	31.1	8	2	Q93SR0_STAEP	Q93sr0 staphylococ
20	14	31.1	9	1	TAL1_PICJA	P17440 pichia jadi
21	14	31.1	9	2	Q7M4R5_HUMAN	Q7m4r5 homo sapien
22	14	31.1	9	2	Q7M471_VESOR	Q7m471 vespa orien
23	14	31.1	9	2	Q9FSZ2_CICAR	Q9fsz2 cicer ariet
24	14	31.1	9	2	Q8CG39_RAT	Q8cg39 rattus norv
25	14	31.1	9	2	Q9QZA8_MOUSE	Q9qza8 mus musculu
26	14	31.1	9	2	Q6Q7G0_RANRI	Q6q7g0 rana ridibu
27	14	31.1	9	2	Q85710_9RETR	Q85710 rous sarcom
28	14	31.1	9	2	Q8UTD7_9HIV1	Q8utd7 human immun
29	13	28.9	7	2	Q66205_9CORO	Q66205 transmissib
30	13	28.9	8	2	Q9HDS4_ASPFL	Q9hds4 aspergillus
31	13	28.9	8	2	Q15889_HUMAN	Q15889 homo sapien
32	13	28.9	8	2	Q7M390_BALAC	Q7m390 balaenopter
33	13	28.9	8	2	Q37854_BPR17	Q37854 bacteriopha
34	13	28.9	8	2	Q6JC68_SOYBN	Q6jc68 glycine max
35	13	28.9	8	2	Q7XB03_MAIZE	Q7xb03 zea mays (m
36	13	28.9	8	2	Q51594_9ZZZZ	Q51594 plasmid col
37	13	28.9	9	2	Q6UVK2_MALDO	Q6uvk2 malus domes
38	13	28.9	9	2	Q7X8P7_MAIZE	Q7x8p7 zea mays (m
39	13	28.9	9	2	Q56SS9_SAMCA	Q56ss9 sambucus ca
40	13	28.9	9	2	Q56ST0_9DIPS	Q56st0 viburnum ut
41	13	28.9	9	2	Q56ST1_9DIPS	Q56st1 viburnum ur
42	13	28.9	9	2	Q56ST2_9DIPS	Q56st2 viburnum tr
43	13	28.9	9	2	Q56ST3_VIBOP	Q56st3 viburnum op
44	13	28.9	9	2	Q56ST4_9DIPS	Q56st4 viburnum ti
45	13	28.9	9	2	Q56ST5_9DIPS	Q56st5 viburnum su

ALIGNMENTS

RESULT 1
Q7R8X5_PLAYO
ID Q7R8X5_PLAYO PRELIMINARY; PRT; 9 AA.
AC Q7R8X5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY07095;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002528; EAA19452.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 9 AA; 1013 MW; 4684D447244441E7 CRC64;

Query Match 42.2%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDL 6
:||::|
Db 1 MLHNNL 6

RESULT 2
Q47556_ECOLI
ID Q47556_ECOLI PRELIMINARY; PRT; 9 AA.
AC Q47556;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Aspartate transcarbamoylase regulatory chain (Fragment).
GN Name=pyrI;

```
OS   Escherichia coli K12.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83333;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82275057; PubMed=7051000;
RA   Pauza C.D., Karels M.J., Navre M., Schachman H.K.;
RT   "Genes encoding Escherichia coli aspartate transcarbamoylase: the
RT   pyrB-pyrI operon.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83195078; PubMed=6302686;
RA   Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
RA   Wild J.R.;
RT   "Nucleotide sequence of the structural gene (pyrB) that encodes the
RT   catalytic polypeptide of aspartate transcarbamoylase of Escherichia
RT   coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
DR   EMBL; J01670; AAA24475.1; -; Genomic_DNA.
FT   NON_TER       9       9
SQ   SEQUENCE   9 AA;  1085 MW;  99EFD723344AA1F1 CRC64;

  Query Match             42.2%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 HDDLLE 8
              ||: |:
Db          3 HDNKLQ 8


RESULT 3
Q28742_RABIT
ID   Q28742_RABIT PRELIMINARY;      PRT;     7 AA.
AC   Q28742;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-myosin heavy chain (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC   Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84221901; PubMed=6328491;
RA   Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jokovcic S.,
RA   Rabinowitz M.;
RT   "Characterization of genomic clones specifying rabbit alpha- and beta-
RT   ventricular myosin heavy chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR   EMBL; K01698; AAA31415.1; -; Genomic_DNA.
DR   PIR; I46868; I46868.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  916 MW;  6B1B1AA1E69326B0 CRC64;

  Query Match             40.0%;  Score 18;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDD 5
              :||:
Db          3 MHDE 6


RESULT 4
Q7M3S5_9TRYP
ID   Q7M3S5_9TRYP PRELIMINARY;      PRT;     9 AA.
AC   Q7M3S5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Phosphoenolpyruvate carboxykinase.
OS   Trypanosoma brucei.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX   NCBI_TaxID=5691;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=95284106; PubMed=7766679; DOI=10.1016/0167-4838(95)00061-X;
RA   Hunt M., Koehler P.;
RT   "Purification and characterization of phosphoenolpyruvate
RT   carboxykinase from Trypanosoma brucei.";
RL   Biochim. Biophys. Acta 1249:15-22(1995).
DR   PIR; S55696; S55696.
SQ   SEQUENCE   9 AA;  1063 MW;  35F2244331E05047 CRC64;

  Query Match             37.8%;  Score 17;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::| :|
Db          3 IIHKNL 8


RESULT 5
O99182_9SMEG
ID   O99182_9SMEG PRELIMINARY;      PRT;     7 AA.
AC   O99182;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytochrome oxidase I (Fragment).
GN   Name=COI;
OS   Gnatholebias zonatus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC   Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX   NCBI_TaxID=135316;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA   Murphy W.J., Thomerson J.E., Collier G.E.;
RT   "Phylogeny of the Neotropical killifish family Rivulidae
RT   (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT   sequences.";
RL   Mol. Phylogenet. Evol. 13:289-301(1999).
DR   EMBL; AF002591; AAD01074.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  899 MW;  672721F6CB572030 CRC64;

  Query Match             35.6%;  Score 16;  DB 2;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLL 7
              :|:  ||
Db          1 ILYQHLL 7


RESULT 6
Q7Z6G0_HUMAN
ID   Q7Z6G0_HUMAN PRELIMINARY;      PRT;     8 AA.
AC   Q7Z6G0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fumarate hydratase (Fragment).
OS   Homo sapiens (Human).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Wei M.-H., Nickerson M.L., Toro J.R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY299638; AAP57532.1; -; Genomic_DNA.
FT   NON_TER      1      1
FT   NON_TER      8      8
SQ   SEQUENCE   8 AA;  881 MW;  40C5B1E732C44330 CRC64;

  Query Match             35.6%;  Score 16;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLH 3
              |||
Db          4 VLH 6


RESULT 7
FAR8_MACRS
ID   FAR8_MACRS     STANDARD;      PRT;     9 AA.
AC   P83281;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   FMRFamide-like neuropeptide FLP8 (VSHNNFLRF-amide).
OS   Macrobrachium rosenbergii (Giant fresh water prawn).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC   Palaemonoidea; Palaemonidae; Macrobrachium.
OX   NCBI_TaxID=79674;
RN   [1]
RP   PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Eyestalk;
RX   MEDLINE=21107394; PubMed=11179812; DOI=10.1016/S0196-9781(00)00382-X;
RA   Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA   Sithigorngul W., Petsom A.;
RT   "Three more novel FMRFamide-like neuropeptide sequences from the
RT   eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL   Peptides 22:191-197(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI; RANGE=1-9; NOTE=Ref.1.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW   Amidation; Direct protein sequencing; Neuropeptide.
FT   MOD_RES      9      9       Phenylalanine amide.
SQ   SEQUENCE   9 AA;  1133 MW;  845A0729C44441F5 CRC64;

  Query Match             35.6%;  Score 16;  DB 1;  Length 9;
  Best Local Similarity   42.9%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLL 7
              | |:: |
Db          1 VSHNNFL 7


RESULT 8
Q70SM2_HUMAN
ID   Q70SM2_HUMAN PRELIMINARY;      PRT;     9 AA.
AC   Q70SM2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypermethylated in cancer 1 (Fragment).
GN   Name=HIC1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Pinte S., Guerardel C., Deltour S., Godwin A.K., Leprince D.;
RT   "Identification of a second G-C-rich promoter conserved in the human,
RT   murine and rat tumor suppressor genes HIC1.";
RL   Oncogene 23:4023-4031(2004).
DR   EMBL; AJ550616; CAD79467.1; -; mRNA.
FT   NON_TER      9      9
SQ   SEQUENCE   9 AA;  964 MW;  5B5E6DDB1681AAA7 CRC64;

  Query Match             35.6%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              | :||
Db          3 DTMEA 7


RESULT 9
Q4X981_PLACH
ID   Q4X981_PLACH PRELIMINARY;      PRT;     9 AA.
AC   Q4X981;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   ORFNames=PC404684.00.0;
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAJ01008648; CAH86543.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   9 AA;  1010 MW;  495F4441E6905727 CRC64;

  Query Match             35.6%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   16.7%;  Pred. No. 2.2e+06;
  Matches    1;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::|:::
Db          4 IMHNNV 9


RESULT 10
Q8LPT5_MAIZE
ID   Q8LPT5_MAIZE PRELIMINARY;      PRT;     9 AA.
```

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AC   Q8LPT5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-expansin-like protein (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA   Morgante M., Rafalski J.A.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY094310; AAM21836.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  977 MW;  5C05B2D2CB1AAAA3 CRC64;

  Query Match             35.6%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              |::::|
Db          4 DEVVDA 9


RESULT 11
P82568_STRPY
ID   P82568_STRPY  PRELIMINARY;      PRT;     9 AA.
AC   P82568;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Unknown protein from 2D-page (Fragment).
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RC   STRAIN=JRS4;
RA   Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA   VanBogelen R.A.;
RT   "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT   proteins.";
RL   Submitted (MAY-2000) to Swiss-Prot.
CC   -!- MASS SPECTROMETRY: MW=22592.04; METHOD=Electrospray.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1069 MW;  2A771042CB1AB2D7 CRC64;

  Query Match             35.6%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              |:::|
Db          4 DEVIE 8


RESULT 12
Q15900_HUMAN
ID   Q15900_HUMAN PRELIMINARY;      PRT;     8 AA.
AC   Q15900;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Homo sapiens (clone XP7B11A) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Placenta;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32079; AAA73890.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  931 MW;  B5DDC403369AAEB1 CRC64;

  Query Match             33.3%;  Score 15;  DB 2;  Length 8;
  Best Local Similarity   42.9%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 HDDLLEA 9
              | |:  |
Db          1 HCDMKRA 7


RESULT 13
Q4XT27_PLACH
ID   Q4XT27_PLACH PRELIMINARY;      PRT;     8 AA.
AC   Q4XT27;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=PC106664.00.0;
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAJ01003387; CAH79935.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   8 AA;  1050 MW;  EFDB01A04B5B11E6 CRC64;

  Query Match             33.3%;  Score 15;  DB 2;  Length 8;
  Best Local Similarity   28.6%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 LHDDLLE 8
              :|: : |
Db          1 MHEYITE 7


RESULT 14
Q9XJN0_9VIRU
ID   Q9XJN0_9VIRU PRELIMINARY;      PRT;     9 AA.
AC   Q9XJN0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P10 (Fragment).
OS   Bacteriophage phi-10.
```

```
OC   Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
OX   NCBI_TaxID=90889;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99350412; PubMed=10419946;
RA   Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
RA   Hoogstraten D.;
RT   "Isolation of additional bacteriophages with genomes of segmented
RT   double-stranded RNA.";
RL   J. Bacteriol. 181:4505-4508(1999).
DR   EMBL; AF125675; AAD22555.1; -; Genomic_RNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1058 MW;  880E376AA720544A CRC64;

  Query Match             33.3%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              |::|:
Db          2 DNILD 6


RESULT 15
TRPI_PSEPU
ID   TRPI_PSEPU     STANDARD;      PRT;     6 AA.
AC   P36414;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
DE   activator) (Fragment).
GN   Name=trpI;
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=PPG1 C1S;
RX   MEDLINE=89335826; PubMed=2503057; DOI=10.1016/0300-9084(89)90183-1;
RA   Eberly L., Crawford I.P.;
RT   "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT   putida.";
RL   Biochimie 71:521-531(1989).
CC   -!- FUNCTION: Activates the expression of the trpBA genes encoding the
CC       two tryptophan synthase subunits. In the absence of the inducer
CC       (indoleglycerol phosphate), trpI binds upstream of the trpAB
CC       operon, overlapping its own promoter region.
CC   -!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X13299; CAA31660.1; -; Genomic_DNA.
DR   InterPro; IPR000847; HTH_LysR.
DR   PROSITE; PS50931; HTH_LYSR; PARTIAL.
KW   Activator; Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW   DNA-binding; Transcription; Transcription regulation;
KW   Tryptophan biosynthesis.
FT   NON_TER       6      6
SQ   SEQUENCE   6 AA;  683 MW;  77672AA1EDD6F000 CRC64;

  Query Match             31.1%;  Score 14;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HD 4
              ||
Db          3 HD 4
```

Search completed: April 6, 2006, 16:25:11
Job time : 119 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:25:31 ; Search time 27.3333 Seconds
(without alignments)
27.222 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	2	US-09-269-250E-20	Sequence 20, Appl
2	45	100.0	9	2	US-09-489-760-2	Sequence 2, Appli
3	37	82.2	9	2	US-09-269-250E-18	Sequence 18, Appl
4	37	82.2	9	2	US-09-489-760-5	Sequence 5, Appli
5	36	80.0	9	2	US-09-269-250E-29	Sequence 29, Appl
6	36	80.0	9	2	US-09-489-760-1	Sequence 1, Appli
7	30	66.7	9	2	US-09-489-760-4	Sequence 4, Appli
8	28.5	63.3	8	2	US-09-269-250E-38	Sequence 38, Appl
9	25	55.6	7	2	US-09-025-819-5	Sequence 5, Appli
10	25	55.6	7	2	US-09-808-126-5	Sequence 5, Appli
11	25	55.6	7	2	US-09-803-951-5	Sequence 5, Appli
12	25	55.6	9	2	US-08-582-333A-3	Sequence 3, Appli
13	25	55.6	9	2	US-09-305-923A-7	Sequence 7, Appli
14	25	55.6	9	2	US-08-946-298-4	Sequence 4, Appli
15	23	51.1	6	2	US-09-217-609A-8	Sequence 8, Appli
16	23	51.1	6	2	US-08-873-235B-8	Sequence 8, Appli
17	23	51.1	9	2	US-08-159-339A-370	Sequence 370, App
18	22	48.9	5	2	US-08-811-463-30	Sequence 30, Appl
19	22	48.9	5	2	US-09-933-497B-30	Sequence 30, Appl
20	22	48.9	7	1	US-08-208-036-7	Sequence 7, Appli
21	22	48.9	7	1	US-08-208-036-9	Sequence 9, Appli
22	22	48.9	7	1	US-08-428-823-7	Sequence 7, Appli
23	22	48.9	7	1	US-08-428-823-9	Sequence 9, Appli
24	22	48.9	7	2	US-08-556-419-14	Sequence 14, Appl
25	22	48.9	7	2	US-09-173-941-82	Sequence 82, Appl
26	22	48.9	7	2	US-09-494-190-82	Sequence 82, Appl
27	22	48.9	8	1	US-08-403-378B-13	Sequence 13, Appl
28	22	48.9	9	2	US-09-217-609A-11	Sequence 11, Appl
29	22	48.9	9	2	US-08-873-235B-11	Sequence 11, Appl
30	21	46.7	6	1	US-08-459-568-20	Sequence 20, Appl
31	21	46.7	6	1	US-08-399-411-20	Sequence 20, Appl
32	21	46.7	6	2	US-08-516-859A-20	Sequence 20, Appl
33	21	46.7	6	2	US-09-586-472-20	Sequence 20, Appl
34	21	46.7	6	2	US-09-528-706-20	Sequence 20, Appl
35	21	46.7	8	1	US-08-459-568-75	Sequence 75, Appl
36	21	46.7	8	1	US-08-399-411-75	Sequence 75, Appl
37	21	46.7	8	2	US-08-516-859A-75	Sequence 75, Appl
38	21	46.7	8	2	US-09-419-826-1	Sequence 1, Appli
39	21	46.7	8	2	US-09-419-826-37	Sequence 37, Appl
40	21	46.7	8	2	US-09-586-472-75	Sequence 75, Appl
41	21	46.7	8	2	US-09-528-706-75	Sequence 75, Appl
42	21	46.7	9	1	US-07-671-757-30	Sequence 30, Appl
43	21	46.7	9	1	US-08-343-602-2	Sequence 2, Appli
44	21	46.7	9	1	US-08-459-568-72	Sequence 72, Appl
45	21	46.7	9	1	US-08-459-568-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen

US-09-489-760-2

Query Match 100.0%; Score 45; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
||||||||| |
Db 1 VLHDDLLEA 9

RESULT 3
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| |||||| |
Db 1 VLRDDLLEA 9

RESULT 4
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA
US-09-489-760-5

Query Match 82.2%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| |||||| |
Db 1 VLRDDLLEA 9

RESULT 5

US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

Query Match 80.0%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| |||||| |
Db 1 VLXDDLLEA 9

RESULT 6
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
; OTHER INFORMATION: RESIDUE
US-09-489-760-1

Query Match 80.0%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| |||||| |
Db 1 VLXDDLLEA 9

RESULT 7
US-09-489-760-4
; Sequence 4, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin

```
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;    LENGTH: 9
;    TYPE: PRT
;    ORGANISM: Histocompatibility antigen
;    FEATURE:
;    NAME/KEY: PEPTIDE
;    LOCATION: (2)..(7)
;    OTHER INFORMATION: AMINO ACIDS X REPRESENT LEUCINE OR ISOLEUCINE
;    OTHER INFORMATION: RESIDUES
US-09-489-760-4

  Query Match             66.7%;  Score 30;  DB 2;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 4.6e+05;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              | |||  ||
Db          1 VXHDDXXEA 9


RESULT 8
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;    LENGTH: 8
;    TYPE: PRT
;    ORGANISM: HUMAN
US-09-269-250E-38

  Query Match             63.3%;  Score 28.5;  DB 2;  Length 8;
  Best Local Similarity   88.9%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 VLHDDLLEA 9
              ||| ||||| 
Db          1 VLH-DLLEA 8


RESULT 9
US-09-025-819-5
; Sequence 5, Application US/09025819
; Patent No. 6225097
;  GENERAL INFORMATION:
;    APPLICANT:  Obata, Shusei
;    APPLICANT:  Nishino, Tokuzo
;    APPLICANT:  Koyama, Tanetoshi
;    APPLICANT:  Sato, Yoshihiro
;    TITLE OF INVENTION:  DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KENYON & KENYON
;      STREET:  1500 K Street, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,819
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 251675
;      FILING DATE:  17-SEP-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Khalilian, Houri
;      REGISTRATION NUMBER:  39,546
;      REFERENCE/DOCKET NUMBER:  10235/2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-220-4200
;      TELEFAX:  202-220-4201
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-025-819-5

  Query Match             55.6%;  Score 25;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              :||||
Db          3 LLHDD 7


RESULT 10
US-09-808-126-5
; Sequence 5, Application US/09808126
; Patent No. 6410280
;   GENERAL INFORMATION:
;        APPLICANT: Obata, Shusei
;                   Nishino, Tokuzo
;                   Koyama, Tanetoshi
;                   Sato, Yoshihiro
;        TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KENYON & KENYON
;             STREET: 1500 K Street, N.W.
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/808,126
;             FILING DATE: 08-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/025,819
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Khalilian, Houri
;             REGISTRATION NUMBER: 39,546
```

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;            REFERENCE/DOCKET NUMBER: 10235/2
;          TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-220-4200
;            TELEFAX: 202-220-4201
;     INFORMATION FOR SEQ ID NO: 5:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 7 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-808-126-5

  Query Match             55.6%;  Score 25;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              :||||
Db          3 LLHDD 7


RESULT 11
US-09-803-951-5
; Sequence 5, Application US/09803951
; Patent No. 6413761
;   GENERAL INFORMATION:
;        APPLICANT: Obata, Shusei
;                   Nishino, Tokuzo
;                   Koyama, Tanetoshi
;                   Sato, Yoshihiro
;        TITLE OF INVENTION: DECAPRENYL DIPHOSPHATE SYNTHETASE GENE
;        NUMBER OF SEQUENCES: 31
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KENYON & KENYON
;             STREET: 1500 K Street, N.W.
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20005
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/803,951
;             FILING DATE: 13-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/025,819
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Khalilian, Houri
;             REGISTRATION NUMBER: 39,546
;             REFERENCE/DOCKET NUMBER: 10235/2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-220-4200
;             TELEFAX: 202-220-4201
;     INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-803-951-5

  Query Match             55.6%;  Score 25;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              :||||
Db          3 LLHDD 7


RESULT 12
US-08-582-333A-3
; Sequence 3, Application US/08582333A
; Patent No. 6255059
;  GENERAL INFORMATION:
;    APPLICANT:  Klein, Christine A.
;    APPLICANT:  Murphy, Andrew J. M.
;    TITLE OF INVENTION:  Methods and Compositions for
;    TITLE OF INVENTION:  Identifying Receptor Effectors
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  AscII(text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/582,333A
;      FILING DATE:  17-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Catherine J. Kara
;      REGISTRATION NUMBER:  41,106
;      REFERENCE/DOCKET NUMBER:  CPI-012CP5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-4214
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-582-333A-3

  Query Match             55.6%;  Score 25;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 4.6e+05;
  Matches    3;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              ::|:|: :|
Db          1 LIHEDIAKA 9


RESULT 13
US-09-305-923A-7
; Sequence 7, Application US/09305923A
; Patent No. 6355473
; GENERAL INFORMATION:
;  APPLICANT: Ostanin, Kirill
;  APPLICANT:  Silverman, Lauren
;  TITLE OF INVENTION: YEAST CELLS HAVING MUTATIONS IN stp22 AND USES THEREFOR
;  FILE REFERENCE: CPI-091
;  CURRENT APPLICATION NUMBER: US/09/305,923A
;  CURRENT FILING DATE:  1999-05-05
;  PRIOR APPLICATION NUMBER: 60/084,420
;  PRIOR FILING DATE: 1998-05-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
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;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-09-305-923A-7

  Query Match             55.6%;  Score 25;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 4.6e+05;
  Matches    3;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              ::|:|: :|
Db          1 LIHEDIAKA 9


RESULT 14
US-08-946-298-4
; Sequence 4, Application US/08946298A
; Patent No. 6864060
; GENERAL INFORMATION:
;  APPLICANT: Fowlkes, Dana M.
;  TITLE OF INVENTION: YEAST CELLS EXPRESSING MODIFIED G PROTEINS AND METHODS
;  TITLE OF INVENTION: OF USE THEREFOR
;  FILE REFERENCE: CPI-012CP8
;  CURRENT APPLICATION NUMBER: US/08/946,298A
;  CURRENT FILING DATE: 1997-10-07
;  EARLIER APPLICATION NUMBER: 08/689,172
;  EARLIER FILING DATE: 1996-08-06
;  EARLIER APPLICATION NUMBER: 08/582,333
;  EARLIER FILING DATE: 1996-01-17
;  EARLIER APPLICATION NUMBER: 08/463,181
;  EARLIER FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: 08/322,137
;  EARLIER FILING DATE: 1994-10-13
;  EARLIER APPLICATION NUMBER: 08/309,313
;  EARLIER FILING DATE: 1994-09-20
;  EARLIER APPLICATION NUMBER: 08/190,328
;  EARLIER FILING DATE: 1994-01-31
;  EARLIER APPLICATION NUMBER: 08/041,431
;  EARLIER FILING DATE: 1993-03-31
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-08-946-298-4

  Query Match             55.6%;  Score 25;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 4.6e+05;
  Matches    3;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              ::|:|: :|
Db          1 LIHEDIAKA 9


RESULT 15
US-09-217-609A-8
; Sequence 8, Application US/09217609A
; Patent No. 6071733
;  GENERAL INFORMATION:
;    APPLICANT:  MURAMATSU, Masayoshi
;    APPLICANT:  KOIKE, Ayumi
;    APPLICANT:  OGURA, Kyozo
;    APPLICANT:  KOYAMA, Tanetoshi
;    APPLICANT:  SHIMIZU, Naoto
;    APPLICANT:  CHO, Yenwin
;    TITLE OF INVENTION:  Prenyl Diphosphate Synthetase Genes
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, NW - Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/217,609A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/873,235
;      FILING DATE:  11-Jun-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TOFFENETTI, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  10235/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-217-609A-8

  Query Match             51.1%;  Score 23;  DB 2;  Length 6;
  Best Local Similarity   60.0%;  Pred. No. 4.6e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDD 5
              ::|||
Db          2 LIHDD 6


Search completed: April  6, 2006, 16:27:38
Job time : 28.6667 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 16:44:31 ; Search time 90.3333 Seconds
(without alignments)
41.629 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	4	US-10-623-176-2	Sequence 2, Appli
2	45	100.0	9	4	US-10-791-217-2	Sequence 2, Appli
3	45	100.0	9	5	US-10-861-335-1	Sequence 1, Appli
4	45	100.0	9	6	US-11-007-740-20	Sequence 20, Appl
5	41	91.1	9	4	US-10-623-176-41	Sequence 41, Appl
6	41	91.1	9	4	US-10-623-176-45	Sequence 45, Appl
7	37	82.2	9	4	US-10-623-176-10	Sequence 10, Appl
8	37	82.2	9	4	US-10-623-176-47	Sequence 47, Appl
9	37	82.2	9	4	US-10-791-217-5	Sequence 5, Appli
10	37	82.2	9	6	US-11-007-740-18	Sequence 18, Appl
11	36	80.0	9	4	US-10-623-176-1	Sequence 1, Appli
12	36	80.0	9	4	US-10-623-176-40	Sequence 40, Appl
13	36	80.0	9	4	US-10-791-217-1	Sequence 1, Appli
14	36	80.0	9	6	US-11-007-740-29	Sequence 29, Appl
15	33	73.3	9	4	US-10-623-176-42	Sequence 42, Appl
16	33	73.3	9	4	US-10-623-176-46	Sequence 46, Appl
17	32	71.1	9	4	US-10-623-176-4	Sequence 4, Appli
18	30	66.7	9	4	US-10-623-176-14	Sequence 14, Appl
19	30	66.7	9	4	US-10-791-217-4	Sequence 4, Appli
20	30	66.7	9	6	US-11-007-740-40	Sequence 40, Appl
21	29	64.4	9	4	US-10-623-176-48	Sequence 48, Appl
22	28.5	63.3	8	4	US-10-623-176-15	Sequence 15, Appl
23	28.5	63.3	8	6	US-11-007-740-38	Sequence 38, Appl
24	28	62.2	9	4	US-10-623-176-23	Sequence 23, Appl
25	28	62.2	9	4	US-10-623-176-38	Sequence 38, Appl
26	28	62.2	9	4	US-10-777-053-95	Sequence 95, Appl
27	28	62.2	9	4	US-10-837-217-95	Sequence 95, Appl
28	27	60.0	9	5	US-10-705-459-280	Sequence 280, App
29	26	57.8	6	4	US-10-166-225A-163	Sequence 163, App
30	26	57.8	6	4	US-10-166-225A-164	Sequence 164, App
31	26	57.8	6	4	US-10-166-225A-165	Sequence 165, App
32	26	57.8	6	4	US-10-166-225A-166	Sequence 166, App
33	26	57.8	9	5	US-10-825-026-48	Sequence 48, Appl
34	25	55.6	6	4	US-10-166-225A-161	Sequence 161, App
35	25	55.6	6	4	US-10-166-225A-162	Sequence 162, App
36	25	55.6	7	3	US-09-803-951-5	Sequence 5, Appli
37	25	55.6	9	3	US-09-747-774A-3	Sequence 3, Appli
38	25	55.6	9	3	US-09-953-354-3	Sequence 3, Appli
39	25	55.6	9	4	US-10-267-074-14	Sequence 14, Appl
40	25	55.6	9	4	US-10-267-074-16	Sequence 16, Appl
41	25	55.6	9	5	US-10-752-478-3	Sequence 3, Appli
42	25	55.6	9	5	US-10-967-087-4	Sequence 4, Appli
43	24	53.3	7	4	US-10-020-354-86	Sequence 86, Appl
44	24	53.3	8	5	US-10-808-187-462	Sequence 462, App
45	24	53.3	8	5	US-10-807-807-462	Sequence 462, App

ALIGNMENTS

RESULT 1
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-2

Query Match 100.0%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
||||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H

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;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

  Query Match             100.0%;  Score 45;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 3
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunot
;  TITLE OF INVENTION:  of tumors
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

  Query Match             100.0%;  Score 45;  DB 5;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 4
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

  Query Match             100.0%;  Score 45;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              |||||||||
Db          1 VLHDDLLEA 9


RESULT 5
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-41

  Query Match             91.1%;  Score 41;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLE 8
              ||||||||
Db          2 VLHDDLLE 9


RESULT 6
US-10-623-176-45
; Sequence 45, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
```

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;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-45

  Query Match             91.1%;  Score 41;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LHDDLLEA 9
              ||||||||
Db          1 LHDDLLEA 8


RESULT 7
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-10

  Query Match             82.2%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 8
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```
US-10-623-176-47
; Sequence 47, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-47

  Query Match             82.2%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 HDDLLEA 9
              |||||||
Db          1 HDDLLEA 7


RESULT 9
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

  Query Match             82.2%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
```

```
Db          1 VLRDDLLEA 9


RESULT 10
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

  Query Match             82.2%;  Score 37;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLRDDLLEA 9


RESULT 11
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   OTHER INFORMATION: wherein X can be R or H
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-1

  Query Match             80.0%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 12
US-10-623-176-40
; Sequence 40, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-40

  Query Match             80.0%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDLL 7
              |||||||
Db          3 VLHDDLL 9


RESULT 13
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
```

; OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

Query Match 80.0%; Score 36; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9
```

RESULT 14
US-11-007-740-29
; Sequence 29, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 2799/58994-A
; CURRENT APPLICATION NUMBER: US/11/007,740
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: 09/269,250
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29

Query Match 80.0%; Score 36; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VLHDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9
```

RESULT 15
US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-42

Query Match 73.3%; Score 33; DB 4; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 VLHDDLLE 8
              || |||||
Db          2 VLRDDLLE 9
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Search completed: April 6, 2006, 16:50:30
Job time : 91.3333 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:46:11 ; Search time 12.3333 Seconds
(without alignments)
22.762 Million cell updates/sec

Title: US-10-791-217A-2
Perfect score: 45
Sequence: 1 VLHDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 38721

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	100.0	9	7	US-11-010-748A-11	Sequence 11, Appl
2	37	82.2	9	7	US-11-010-748A-12	Sequence 12, Appl
3	26	57.8	6	7	US-11-129-143-163	Sequence 163, App
4	26	57.8	6	7	US-11-129-143-164	Sequence 164, App
5	26	57.8	6	7	US-11-129-143-165	Sequence 165, App
6	26	57.8	6	7	US-11-129-143-166	Sequence 166, App
7	25	55.6	6	7	US-11-129-143-161	Sequence 161, App
8	25	55.6	6	7	US-11-129-143-162	Sequence 162, App
9	24	53.3	8	7	US-11-004-399-1155	Sequence 1155, Ap
10	23	51.1	6	6	US-10-485-788A-353	Sequence 353, App
11	23	51.1	7	6	US-10-485-788A-354	Sequence 354, App
12	23	51.1	8	6	US-10-485-788A-355	Sequence 355, App
13	23	51.1	9	7	US-11-033-039-785	Sequence 785, App
14	23	51.1	9	7	US-11-033-039-809	Sequence 809, App
15	22	48.9	5	6	US-10-485-788A-352	Sequence 352, App
16	22	48.9	6	6	US-10-857-435A-443	Sequence 443, App
17	22	48.9	7	6	US-10-982-440-126	Sequence 126, App
18	22	48.9	8	7	US-11-045-024-444	Sequence 444, App
19	22	48.9	8	7	US-11-045-024-5467	Sequence 5467, Ap
20	22	48.9	8	7	US-11-045-024-7094	Sequence 7094, Ap
21	22	48.9	9	7	US-11-045-024-607	Sequence 607, App
22	22	48.9	9	7	US-11-045-024-3715	Sequence 3715, Ap
23	22	48.9	9	7	US-11-045-024-5511	Sequence 5511, Ap
24	22	48.9	9	7	US-11-045-024-12585	Sequence 12585, A
25	22	48.9	9	7	US-11-045-024-14029	Sequence 14029, A
26	21	46.7	4	6	US-10-485-788A-351	Sequence 351, App
27	21	46.7	7	6	US-10-510-155-28	Sequence 28, Appl
28	20	44.4	4	6	US-10-667-295-263	Sequence 263, App
29	20	44.4	4	6	US-10-857-435A-366	Sequence 366, App
30	20	44.4	4	7	US-11-019-027-5	Sequence 5, Appli
31	20	44.4	4	7	US-11-174-413-64	Sequence 64, Appl
32	20	44.4	4	7	US-11-108-088-69	Sequence 69, Appl
33	20	44.4	4	7	US-11-033-030-3	Sequence 3, Appli
34	20	44.4	5	7	US-11-129-143-168	Sequence 168, App
35	20	44.4	5	7	US-11-129-143-169	Sequence 169, App
36	20	44.4	5	7	US-11-129-143-170	Sequence 170, App
37	20	44.4	5	7	US-11-129-143-171	Sequence 171, App
38	20	44.4	5	7	US-11-129-143-172	Sequence 172, App
39	20	44.4	5	7	US-11-129-143-173	Sequence 173, App
40	20	44.4	6	6	US-10-857-435A-367	Sequence 367, App
41	20	44.4	6	6	US-10-857-435A-397	Sequence 397, App
42	20	44.4	6	6	US-10-857-435A-667	Sequence 667, App
43	20	44.4	8	7	US-11-021-305-62	Sequence 62, Appl
44	20	44.4	8	7	US-11-021-305-65	Sequence 65, Appl
45	20	44.4	8	7	US-11-021-305-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-11

Query Match 100.0%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|||||||||
Db 1 VLHDDLLEA 9

RESULT 2
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
; OTHER INFORMATION: ell epitopes
US-11-010-748A-12

Query Match 82.2%; Score 37; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHDDLLEA 9
|| ||||||
Db 1 VLRDDLLEA 9

RESULT 3
US-11-129-143-163
; Sequence 163, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-129-143-163

Query Match 57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDL 6
:||||
Db 1 IHDDL 5

RESULT 4
US-11-129-143-164
; Sequence 164, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-129-143-164

Query Match 57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDL 6
:||||
Db 1 IHDDL 5

RESULT 5
US-11-129-143-165
; Sequence 165, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-129-143-165

Query Match 57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDL 6
:||||
Db 1 IHDDL 5

RESULT 6
US-11-129-143-166
; Sequence 166, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 6
; TYPE: PRT

; ORGANISM: Haemophilus influenzae
US-11-129-143-166

Query Match 57.8%; Score 26; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDL 6
:||||
Db 1 IHDDL 5

RESULT 7
US-11-129-143-161
; Sequence 161, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
US-11-129-143-161

Query Match 55.6%; Score 25; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDL 6
:||||
Db 1 VHDDL 5

RESULT 8
US-11-129-143-162
; Sequence 162, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-162

Query Match 55.6%; Score 25; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDDL 6
:||||
Db 1 VHDDL 5

RESULT 9
US-11-004-399-1155
; Sequence 1155, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1155
; LENGTH: 8
; TYPE: PRT
; ORGANISM: SARS-CoV Virus
US-11-004-399-1155

Query Match 53.3%; Score 24; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LHDD 5
||||
Db 3 LHDD 6

RESULT 10
US-10-485-788A-353
; Sequence 353, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 353
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-353

Query Match 51.1%; Score 23; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHDDL 6
::|||:
Db 1 LVHDDV 6

```
RESULT 11
US-10-485-788A-354
; Sequence 354, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 354
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-354

  Query Match             51.1%;  Score 23;  DB 6;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::|||:
Db          2 LVHDDV 7


RESULT 12
US-10-485-788A-355
; Sequence 355, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 355
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-355

  Query Match             51.1%;  Score 23;  DB 6;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLHDDL 6
              ::|||:
Db          3 LVHDDV 8


RESULT 13
US-11-033-039-785
; Sequence 785, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2017US01
;  CURRENT APPLICATION NUMBER: US/11/033,039
;  CURRENT FILING DATE:  2005-01-11
;  PRIOR APPLICATION NUMBER: 10/245,871
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 1452
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 785
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Zaire ebolavirus
US-11-033-039-785

  Query Match             51.1%;  Score 23;  DB 7;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              :||:  |:|
Db          1 LLHESTLKA 9


RESULT 14
US-11-033-039-809
; Sequence 809, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
;  APPLICANT: HUMPHREYS, ROBERT
;  APPLICANT:  XU, MINZHEN
;  TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
;  FILE REFERENCE: REH-2017US01
;  CURRENT APPLICATION NUMBER: US/11/033,039
;  CURRENT FILING DATE:  2005-01-11
;  PRIOR APPLICATION NUMBER: 10/245,871
;  PRIOR FILING DATE: 2002-09-17
;  PRIOR APPLICATION NUMBER: 10/197,000
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: 09/396,813
;  PRIOR FILING DATE: 1999-09-14
;  NUMBER OF SEQ ID NOS: 1452
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 809
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Zaire ebolavirus
US-11-033-039-809

  Query Match             51.1%;  Score 23;  DB 7;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLHDDLLEA 9
              :||:  |:|
Db          1 LLHESTLKA 9


RESULT 15
US-10-485-788A-352
; Sequence 352, Application US/10485788A
```

; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-352

Query Match 48.9%; Score 22; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 LHDDL 6
              :|||:
Db          1 VHDDV 5
```

Search completed: April 6, 2006, 16:51:13
Job time : 13.3333 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:12:46 ; Search time 111.667 Seconds
(without alignments)
35.413 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	2	AAW99197	Aaw99197 Minor his
2	42	100.0	9	2	AAW97374	Aaw97374 HA-1 R-al
3	42	100.0	9	8	ADH40334	Adh40334 Human min
4	37	88.1	9	2	AAW99196	Aaw99196 Minor his
5	37	88.1	9	2	AAW97375	Aaw97375 HA-1 H-al
6	37	88.1	9	8	ADH40333	Adh40333 Human min
7	36	85.7	9	2	AAW99195	Aaw99195 Minor his
8	36	85.7	9	2	AAW97572	Aaw97572 T-cell ep
9	29	69.0	9	8	ADT73023	Adt73023 Human RSV
10	27	64.3	9	2	AAW47427	Aaw47427 Prenyl di
11	26	61.9	9	8	ADT73690	Adt73690 Human RSV
12	26	61.9	9	8	ADT72767	Adt72767 Human RSV
13	25	59.5	9	5	AAU71428	Aau71428 Human MHC
14	25	59.5	9	8	ADT72766	Adt72766 Human RSV
15	25	59.5	9	8	ADT73689	Adt73689 Human RSV
16	24	57.1	7	4	AAB81550	Aab81550 Zif268 zi
17	24	57.1	9	7	ADM18256	Adm18256 C trachom
18	24	57.1	9	7	ADM18218	Adm18218 Chlamydia
19	23	54.8	9	5	AAU71211	Aau71211 Human MHC
20	23	54.8	9	6	ABR19981	Abr19981 Human can
21	23	54.8	9	6	ABR19426	Abr19426 Human can
22	23	54.8	9	6	ABR18988	Abr18988 Human can
23	23	54.8	9	6	ABR19578	Abr19578 Human can
24	23	54.8	9	6	ABR19174	Abr19174 Human can
25	23	54.8	9	6	ABR19780	Abr19780 Human can
26	23	54.8	9	8	ADU99853	Adu99853 BCZ4 tumo
27	23	54.8	9	8	ABY01546	Aby01546 SARS coro
28	23	54.8	9	9	ADZ50925	Adz50925 Y. pestis
29	22	52.4	9	2	AAW97373	Aaw97373 Peptide e
30	22	52.4	9	8	ADF72091	Adf72091 Rabbit pe
31	22	52.4	9	8	ABY01413	Aby01413 SARS coro
32	22	52.4	9	9	ADW23047	Adw23047 SARS coro
33	21	50.0	4	9	AEB31418	Aeb31418 Endoplasm
34	21	50.0	6	3	AAB12035	Aab12035 Peptide #
35	21	50.0	6	5	AAU80810	Aau80810 Rat Rb-in
36	21	50.0	6	7	ADE84629	Ade84629 Mammalia
37	21	50.0	7	5	ABP48411	Abp48411 Zinc fing
38	21	50.0	7	5	ABP48414	Abp48414 Zinc fing
39	21	50.0	7	5	ABP48419	Abp48419 Zinc fing
40	21	50.0	7	5	ABG79371	Abg79371 CXCR zinc
41	21	50.0	7	6	ABP96179	Abp96179 Zinc fing
42	21	50.0	7	7	ADA62240	Ada62240 Zinc fing
43	21	50.0	7	7	ADA62237	Ada62237 Zinc fing
44	21	50.0	7	7	ADA62245	Ada62245 Zinc fing
45	21	50.0	7	7	ADM20449	Adm20449 Synthetic

ALIGNMENTS

RESULT 1
AAW99197
ID AAW99197 standard; peptide; 9 AA.
XX
AC AAW99197;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #3.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Disclosure; Page 15; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

```
  Query Match            100.0%;  Score 42;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9
```

RESULT 2
AAW97374
ID AAW97374 standard; protein; 9 AA.
XX
AC AAW97374;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 R-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 13; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 R-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC anti-idiotypic B cells and/or T cells and antibodies
XX
SQ Sequence 9 AA;

```
  Query Match            100.0%;  Score 42;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9
```

RESULT 3
ADH40334
ID ADH40334 standard; peptide; 9 AA.
XX
AC ADH40334;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS Homo sapiens.
XX
PN WO2003106692-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-EP006251.
XX
PR 13-JUN-2002; 2002EP-00013423.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Strittmatter W, Moll H;
XX
DR WPI; 2004-082200/08.
XX
PT Providing allelic variant epitope of protein based on single nucleotide
PT polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.
XX
PS Disclosure; Page 82; 119pp; English.
XX
CC The invention relates to a novel method for providing epitopes of allelic
CC variants of antigenic proteins from specific species based on single
CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC subset, screening database of DNA encoding target protein, identifying,
CC selecting allelic peptide/protein variants, expression product or its
CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC selecting epitopes binding to MHC protein. A protein of the invention has
CC cytostatic activity, and may have a use in a vaccine. The method is
CC useful for generating a SNP profile of one or more individuals from a
CC given species by applying the method for several protein from the
CC individuals, where the SNP profile was related to disease, preferably
CC cancer. This is useful for diagnosing a disease in an individual by
CC generating the SNP-related polymorphic profile. A method of the invention
CC is useful for transplanting haematopoietic stem cells from a donor to a
CC recipient and treating cancer, preferably leukaemia, and for determining
CC the progression, regression or onset of a treated disease. The present
CC sequence is used in the exemplification of the invention.
XX
SQ Sequence 9 AA;

```
  Query Match            100.0%;  Score 42;  DB 8;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9
```

RESULT 4
AAW99196
ID AAW99196 standard; peptide; 9 AA.
XX
AC AAW99196;
XX
DT 20-MAY-1999 (first entry)
XX
DE Minor histocompatibility antigen HA-1 T-cell epitope #2.
XX
KW Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW diagnosis; aplastic anaemia; immune deficiency disease.

XX
OS Homo sapiens.
XX
PN WO9905174-A1.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-NL000425.
XX
PR 23-JUL-1997; 97EP-00202303.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy EAJM, Hunt DF, Engelhard VH;
XX
DR WPI; 1999-153312/13.
XX
PT A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT diseases and prevent rejection and host versus graft disease in bone
PT marrow and organ transplantation.
XX
PS Claim 3; Page 32; 47pp; English.
XX
CC The present sequence represents a new peptide (P1) constituting a T-cell
CC epitope obtainable from the minor histocompatibility antigen HA-1. The
CC peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC as a medicine, to induce tolerance for transplants, prevent rejection
CC and/or graft versus host disease, or to treat (auto) immune diseases. In
CC particular it can be used with bone marrow transplantation, in the
CC treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC diseases
XX
SQ Sequence 9 AA;

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 5
AAW97375
ID AAW97375 standard; protein; 9 AA.
XX
AC AAW97375;
XX
DT 13-MAY-1999 (first entry)
XX
DE HA-1 H-allele sequence.
XX
KW Intron; minor histocompatibility antigen HA-1; typing allele; H allele;
KW R allele; polymorphic nucleotide; HA-1 typing; bone marrow transplant;
KW severe aplastic anaemia; leukaemia; immune deficiency disease; ss.
XX
OS Homo sapiens.
XX
PN WO9905313-A2.
XX
PD 04-FEB-1999.
XX
PF 23-JUL-1998; 98WO-EP004928.
XX
PR 23-JUL-1997; 97EP-00202303.
PR 02-JUN-1998; 98EP-00870125.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Goulmy E;
XX
DR WPI; 1999-142960/12.
XX
PT Typing minor histocompatibility antigen HA-1 - by amplifying and
PT identifying HA-1 R and HA-1 H alleles of HA-1, used for, e.g. detection
PT of genetic aberrances.
XX
PS Claim 18; Fig 5; 59pp; English.
XX
CC The present sequence represents part of the minor histocompatibility
CC antigen HA-1 H-allele. The specification describes methods for typing
CC alleles (preferably the H and R alleles) of the minor histocompatibility
CC antigen HA-1 in a sample, which comprise detecting polymorphic
CC nucleotides in the cDNA or genomic nucleic acids of the alleles. The
CC methods can be used for HA-1 typing for bone marrow transplants, severe
CC aplastic anaemia, leukaemia and immune deficiency diseases, as well as
CC detection of genetic aberrances. The probes and primers of the invention
CC can be used to screen for the HA-1 alleles. The HA-1 peptides can be used
CC anti-idiotypic B cells and/or T cells and antibodies
XX
SQ Sequence 9 AA;

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| ||||||
Db 1 VLHDDLLEA 9

RESULT 6
ADH40333
ID ADH40333 standard; peptide; 9 AA.
XX
AC ADH40333;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human minor histocomptibility antigen HA-1 T cell eptiope.
XX
KW human; cytostatic; vaccine; SNP profile; cancer; leukaemia;
KW minor histocomptibility antigen; mHAg; T cell epitope.
XX
OS Homo sapiens.
XX
PN WO2003106692-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-EP006251.
XX
PR 13-JUN-2002; 2002EP-00013423.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Strittmatter W, Moll H;
XX
DR WPI; 2004-082200/08.
XX
PT Providing allelic variant epitope of protein based on single nucleotide
PT polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.
XX
PS Disclosure; Page 82; 119pp; English.
XX
CC The invention relates to a novel method for providing epitopes of allelic
CC variants of antigenic proteins from specific species based on single
CC nucleotide polymorphism (SNP), by defining target protein/peptide or its
CC subset, screening database of DNA encoding target protein, identifying,
CC selecting allelic peptide/protein variants, expression product or its
CC fragment encoded by DNA sequence having SNP, creating variant epitopes,
CC selecting epitopes binding to MHC protein. A protein of the invention has
CC cytostatic activity, and may have a use in a vaccine. The method is

```
CC   useful for generating a SNP profile of one or more individuals from a
CC   given species by applying the method for several protein from the
CC   individuals, where the SNP profile was related to disease, preferably
CC   cancer. This is useful for diagnosing a disease in an individual by
CC   generating the SNP-related polymorphic profile. A method of the invention
CC   is useful for transplanting haematopoietic stem cells from a donor to a
CC   recipient and treating cancer, preferably leukaemia, and for determining
CC   the progression, regression or onset of a treated disease. The present
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 9 AA;

  Query Match             88.1%;  Score 37;  DB 8;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 7
AAW99195
ID   AAW99195 standard; peptide; 9 AA.
XX
AC   AAW99195;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Minor histocompatibility antigen HA-1 T-cell epitope #1.
XX
KW   Minor histocompatibility antigen; HA-1; T-cell epitope; immunological;
KW   graft versus host disease; bone marrow transplant; leukaemia; vaccine;
KW   diagnosis; aplastic anaemia; immune deficiency disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /label= His, Arg
XX
PN   WO9905174-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000425.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-153312/13.
XX
PT   A new minor histocompatibility antigen, HA-1 - useful to treat immune
PT   diseases and prevent rejection and host versus graft disease in bone
PT   marrow and organ transplantation.
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The present sequence represents a new peptide (P1) constituting a T-cell
CC   epitope obtainable from the minor histocompatibility antigen HA-1. The
CC   peptide is immunogenic and can be used as part of a vaccine. P1 is used
CC   as a medicine, to induce tolerance for transplants, prevent rejection
CC   and/or graft versus host disease, or to treat (auto) immune diseases. In
CC   particular it can be used with bone marrow transplantation, in the
CC   treatment of severe aplastic anaemia, leukaemia, and immune deficiency
CC   diseases
XX
SQ   Sequence 9 AA;

  Query Match             85.7%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 8
AAW97572
ID   AAW97572 standard; peptide; 9 AA.
XX
AC   AAW97572;
XX
DT   20-MAY-1999  (first entry)
XX
DE   T-cell epitope from the minor histocompatibility antigen HA-1.
XX
KW   T-cell epitope; minor histocompatibility antigen HA-1; vaccine;
KW   transplant rejection; Graft-versus-Host Disease; autoimmune disease;
KW   neoplastic haematopoietic cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /note= "His or Arg"
XX
PN   WO9905173-A1.
XX
PD   04-FEB-1999.
XX
PF   23-JUL-1998;   98WO-NL000424.
XX
PR   23-JUL-1997;   97EP-00202303.
XX
PA   (UYLE-) RIJKSUNIV LEIDEN.
XX
PI   Goulmy EAJM,  Hunt DF,  Engelhard VH;
XX
DR   WPI; 1999-142855/12.
XX
PT   Immunogenic peptide from minor histocompatibility antigen HA-1 - useful
PT   for inducing tolerance to transplants and prevent rejection or graft-
PT   versus-host disease.
XX
PS   Claim 1; Page 39; 57pp; English.
XX
CC   The present sequence represents an immunogenic peptide constituting a T-
CC   cell epitope, obtainable from the minor histocompatibility antigen HA-1.
CC   The peptide can be used in vaccines or pharmaceutical formulations as
CC   medicines to induce tolerance for transplants so as to prevent rejection
CC   and/or Graft-versus-Host Disease, or to treat autoimmune diseases.
CC   Neoplastic haematopoietic cells presenting the peptides, in an HLA class
CC   I context, can be eliminated after specific recognition of the peptides.
CC   The peptides can also be used to raise antibodies, T-cell receptor, B-
CC   and T-cells
XX
SQ   Sequence 9 AA;

  Query Match             85.7%;  Score 36;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 9
ADT73023
ID   ADT73023 standard; peptide; 9 AA.
```

XX
AC ADT73023;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 919.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 16; SEQ ID NO 919; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 69.0%; Score 29; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
:::||:| |
Db 1 IIKDDILSA 9

RESULT 10
AAW47427
ID AAW47427 standard; peptide; 9 AA.
XX
AC AAW47427;
XX
DT 05-JUN-1998 (first entry)
XX
DE Prenyl diphosphate synthetase preserved region VI sequence.
XX
KW Prenyl diphosphate synthetase; polyprenyl diphosphate; vitamin K;
KW ubiquinone; preserved region VI.
XX
OS Synthetic.
XX
PN EP812914-A2.
XX
PD 17-DEC-1997.
XX
PF 13-JUN-1997; 97EP-00109692.
XX
PR 14-JUN-1996; 96JP-00154441.
XX
PA (TOYT) TOYOTA JIDOSHA KK.
XX
PI Muramatsu M, Koike A, Ogura K, Koyama T, Shimizu N, Cho Y;
XX
DR WPI; 1998-034975/04.
XX
PT DNA encoding prenyl diphosphate synthetase subunit(s) - new Micrococcus
PT prenyl diphosphate synthetase subunit polypeptide(s), and methods for
PT preparing enzymes from subunit(s).
XX
PS Example 2; Page 26; 46pp; English.
XX
CC The present sequence from preserved region VI of prenyl diphosphate
CC synthetase (PDS), was used in the preparation of primers for the
CC amplification of PDS DNA. Substances synthesised by PDS, i.e. polyprenyl
CC diphosphates, are precursors of physiologically active substances, e.g.
CC vitamin K and ubiquinones
XX
SQ Sequence 9 AA;

Query Match 64.3%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LRDDLLE 8
:|||:|:
Db 3 IRDDILD 9

RESULT 11
ADT73690
ID ADT73690 standard; peptide; 9 AA.
XX
AC ADT73690;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 1586.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N

PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 16; SEQ ID NO 1586; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 61.9%; Score 26; DB 8; Length 9;
Best Local Similarity 44.4%; Pred. No. 2e+06;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
:::||:| |
Db 1 IIKDDILLA 9

RESULT 12
ADT72767
ID ADT72767 standard; peptide; 9 AA.
XX
AC ADT72767;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 663.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Disclosure; SEQ ID NO 663; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 61.9%; Score 26; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LRDDLLEA 9
::||:| |
Db 1 IKDDILSA 8

RESULT 13
AAU71428
ID AAU71428 standard; peptide; 9 AA.
XX
AC AAU71428;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human MHC molecule HLA-A11 binding 103P3E8 peptide #35.
XX
KW 103P3E8; prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
KW tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW chromosome 9q13-q21.
XX
OS Homo sapiens.
XX
PN WO200179557-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US012181.
XX
PR 12-APR-2000; 2000US-0196647P.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Faris M, Challita-Eid PM, Raitano AB, Mitchell SC, Afar DEH;
PI Jakobovits A;
XX
DR WPI; 2002-061976/08.
XX
PT Monitoring 103P3E8 gene products in sample from patient (suspected of)
PT having cancer, useful for diagnosing, managing or treating cancers, e.g.
PT prostate cancer, comprises determining presence of aberrant 103P3E8 gene
PT products.
XX
PS Disclosure; Page 90; 128pp; English.
XX
CC Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and
CC peptide fragments of the protein. 103P3E8 exhibits tissue specific
CC expression in normal adult tissue, but it is also aberrantly expressed in

CC many cancers including tumours of the prostate, bladder, kidney, colon,
CC lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related
CC protein and peptide fragments and specific PCR primers are therefore
CC useful for diagnosing and treating cancer. A vector comprising a
CC polynucleotide which encodes a single chain monoclonal antibody, that
CC immunospecifically binds to an 103P3E8-related protein, and a ribozyme
CC capable of cleaving a polynucleotide having the 103P3E8 coding sequence,
CC are both useful in the preparation of a composition for treating a
CC patient with a cancer that expresses 103P3E8. The sequences can be used
CC in diagnostic methods to monitor the level of 103P3E8 gene products in
CC serum, blood, urine and tissue and to thereby detect the presence of
CC cancerous cells
XX
SQ Sequence 9 AA;

Query Match 59.5%; Score 25; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LRDDLLEA 9
:: |||||
Db 2 VKKDLLEA 9

RESULT 14
ADT72766
ID ADT72766 standard; peptide; 9 AA.
XX
AC ADT72766;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 662.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Disclosure; SEQ ID NO 662; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 59.5%; Score 25; DB 8; Length 9;
Best Local Similarity 42.9%; Pred. No. 2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLL 7
:::||:|
Db 2 IIKDDIL 8

RESULT 15
ADT73689
ID ADT73689 standard; peptide; 9 AA.
XX
AC ADT73689;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human RSV L high affinity binding peptide SeqID 1585.
XX
KW human respiratory syncytial virus; cytotoxic T lymphocyte; CTL;
KW MHC epitope; DNA-based immunisation; RSV infection; virucidal; vaccine.
XX
OS Human respiratory syncytial virus.
XX
PN WO2004092207-A2.
XX
PD 28-OCT-2004.
XX
PF 16-APR-2004; 2004WO-EP004061.
XX
PR 16-APR-2003; 2003EP-00447095.
XX
PA (ALGO-) ALGONOMICS NV.
XX
PI Lasters I, Desmet J, Stegmann T;
XX
DR WPI; 2004-758334/74.
XX
PT New respiratory syncytial virus (RSV) peptides (e.g. G, M, M2-1, M2-2, N
PT or P) for inducing an immune response to RSV or for diagnosing,
PT preventing or treating viral infections, particularly RSV infection.
XX
PS Claim 16; SEQ ID NO 1585; 143pp; English.
XX
CC This invention relates to novel isolated or purified peptides of the
CC human respiratory syncytial virus (RSV), in particular ten RSV genes
CC encoding 11 separate viral proteins: non-structural proteins NS-1 (also
CC known as the 1C protein) & NS-2 (1B protein), a polymerase protein L and
CC eight structural proteins preferably G, also M, M2-1, M2-2, N, P, F, and
CC SH (also known as the 1A protein). Specifically, it refers to a
CC composition comprising an above peptide mixed with a pharmaceutical
CC excipient or an RSV immunogenic composition comprising a recombinant
CC expression vector with a nucleic acid insert encoding an above peptide.
CC The present invention describes an in vitro method of detecting cytotoxic
CC T lymphocytes (CTLs) that respond to a major histocompatibility complex
CC (MHC) class I restricted T-cell stimulating peptide epitope of RSV. The
CC RSV peptide is useful for preparing a diagnostic composition or an RSV
CC (prophylactic or therapeutic) vaccine composition for a DNA-based
CC immunisation, or for preparing an immune response provoking vaccine in
CC the event of RSV infection (the vaccine being prepared by contacting the
CC polypeptide in an immune response-provoking amount of specific CTL).
CC Accordingly, these peptide compositions have virucidal activity. This
CC peptide sequence is a human RSV high binding affinity peptide of the
CC invention.

XX
SQ Sequence 9 AA;

Query Match 59.5%; Score 25; DB 8; Length 9;
Best Local Similarity 42.9%; Pred. No. 2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VLRDDLL 7
              :::||:|
Db          2 IIKDDIL 8
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Search completed: April 6, 2006, 16:19:10
Job time : 112.667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:19:36 ; Search time 18.6667 Seconds
(without alignments)
46.390 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	16	38.1	7	2	S68004	hucolin, 75K chain
2	16	38.1	8	2	PC4131	hypothetical prote
3	15	35.7	7	2	A59489	protein kinase C i
4	14	33.3	7	2	S20446	elastase - Pseudom
5	14	33.3	9	2	A60427	macrophage cytotox
6	13	31.0	9	2	PH0942	T-cell receptor be
7	12	28.6	4	2	I40697	biotin A - Citroba
8	12	28.6	5	2	PT0679	T-cell receptor be
9	12	28.6	5	2	PT0601	T-cell receptor be
10	12	28.6	6	2	B35640	cerebellar degener
11	12	28.6	6	2	PT0533	T-cell receptor be
12	12	28.6	7	2	A34026	acetylcholinestera
13	12	28.6	7	2	B39040	calsequestrin, fas
14	12	28.6	7	2	PT0628	T-cell receptor be
15	12	28.6	7	2	PT0722	T-cell receptor be
16	12	28.6	7	2	PT0576	T-cell receptor be
17	12	28.6	8	2	PT0557	T-cell receptor be
18	12	28.6	8	2	A61328	trypsin (EC 3.4.21
19	12	28.6	9	2	PH0108	late G1-69 protein
20	12	28.6	9	2	PT0562	T-cell receptor be
21	12	28.6	9	2	B30572	T-cell receptor be
22	12	28.6	9	2	A39841	sucrose 3-glucosyl
23	12	28.6	9	2	A37027	macrophage chemota
24	11	26.2	5	2	D60274	major protein anti
25	11	26.2	6	2	T11779	phosphoglycerate t
26	11	26.2	7	2	S25266	pilE protein - Esc
27	11	26.2	7	2	PT0602	T-cell receptor be
28	11	26.2	8	2	S22428	chitin-binding pro
29	11	26.2	8	2	B33099	158K exoantigen -
30	11	26.2	8	2	S69165	ferredoxin a2 - Ja
31	11	26.2	9	2	S66419	tetrameric protein
32	11	26.2	9	2	B28495	conopressin S - co
33	11	26.2	9	2	PW0002	chlorophyll a/b-bi
34	11	26.2	9	2	B39841	dextransucrase (EC
35	11	26.2	9	2	PS0253	glycine cleavage s
36	11	26.2	9	2	A12872	transaldolase (EC
37	11	26.2	9	2	B57444	neuropeptide Grb-A
38	11	26.2	9	2	C57444	neuropeptide Grb-A
39	11	26.2	9	2	A44787	calliFMRFamide 10
40	10	23.8	4	2	A48360	gamma subunit of P
41	10	23.8	4	2	A26209	protein-glutamine
42	10	23.8	4	2	A35779	neuropeptide Antho
43	10	23.8	6	2	B44510	hypothetical prote
44	10	23.8	6	2	H48394	glycoprotein compo
45	10	23.8	7	2	S78024	ribosomal protein

ALIGNMENTS

RESULT 1
S68004
hucolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
R;Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A;Reference number: S68004; MUID:96087107; PMID:7498469
A;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>
A;Cross-references: UNIPARC:UPI000017C164

Query Match 38.1%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
|||
Db 4 DDL 6

RESULT 2
PC4131
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: PC4131
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding
y for biosynthesis of heme d1.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
A;Accession: PC4131
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <KAW>
A;Cross-references: UNIPROT:P95412; UNIPARC:UPI000017A96A; DDBJ:D50473; NID:g1217594
A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0
C;Superfamily: Pseudomonas stutzeri nirD protein

Query Match 38.1%; Score 16; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
|||
Db 2 DDL 4

```
RESULT 3
A59489
protein kinase C inhibitor - rat (fragment)
C;Species: Rattus norvegicus
C;Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 25-Aug-2003
C;Accession: A59489
R;Negoro, M.
submitted to the Protein Sequence Database, June 2003
A;Description: Purification of PKCI from rat liver.
A;Reference number: A59489
A;Accession: A59489
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NEG>
A;Experimental source: strain Wistar, liver
A;Note: p-Hydroxyacetophenone-Sepharose binding protein

  Query Match             35.7%;  Score 15;  DB 2;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLRDD 5
              :  ||
Db          2 IFEDD 6


RESULT 4
S20446
elastase - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C;Accession: S20446
R;Kessler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
FEBS Lett. 299, 291-293, 1992
A;Title: Identification of cleavage sites involved in proteolytic processing of Pseudomo
A;Reference number: S20446; MUID:92183956; PMID:1544509
A;Accession: S20446
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <KES>
A;Cross-references: UNIPARC:UPI000017A95F

  Query Match             33.3%;  Score 14;  DB 2;  Length 7;
  Best Local Similarity   50.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLE 8
              ||::
Db          3 DLID 6


RESULT 5
A60427
macrophage cytotoxicity-inducing factor, 29K - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60427
R;Jones, C.M.; Prince, C.A.; Williams, J.S.
Exp. Hematol. 19, 704-709, 1991
A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin
A;Reference number: A60427; MUID:91372335; PMID:1909970
A;Accession: A60427
A;Molecule type: protein
A;Residues: 1-9 <JON>
A;Cross-references: UNIPROT:Q7M4R5; UNIPARC:UPI0000142BE0
A;Note: the sequence from the text on page 706 is inconsistent with that from page 708 i
C;Keywords: cytokine

  Query Match             33.3%;  Score 14;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRD 4
              || |
Db          4 VLED 7


RESULT 6
PH0942
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0942
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0942
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Cross-references: UNIPARC:UPI000017C9DD
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon TGC for residue 2 as Ala
C;Keywords: T-cell receptor

  Query Match             31.0%;  Score 13;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 LLE 8
              |||
Db          5 LLE 7


RESULT 7
I40697
biotin A - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40697
R;Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A;Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacte
A;Reference number: I40697; MUID:89006280; PMID:2971595
A;Accession: I40697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: UNIPROT:P13071; UNIPARC:UPI000017AA21; GB:M21922; NID:g144434

  Query Match             28.6%;  Score 12;  DB 2;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DD 5
              ||
Db          3 DD 4


RESULT 8
PT0679
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0679
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPARC:UPI000017C84D
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
```

A;Accession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C84D
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 4 DD 5

RESULT 9
PT0601
T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0601; PT0617; PT0694
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0601
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPROT:Q64512; UNIPARC:UPI000017C7E6
A;Experimental source: newborn thymus, strain BALB/c, clone 120-2K
A;Accession: PT0617
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FE3>
A;Cross-references: UNIPARC:UPI000017C7E6
A;Experimental source: newborn thymus, strain BALB/c, 120-2CA
A;Accession: PT0694
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FE2>
A;Cross-references: UNIPARC:UPI000017C7E6
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H
C;Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 4 DD 5

RESULT 10
B35640
cerebellar degeneration-related protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C;Accession: B35640
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.B
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal mar
A;Reference number: A35640; MUID:90222173; PMID:2326268
A;Accession: B35640
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6 <CHE>
A;Cross-references: UNIPARC:UPI000017C63A

Query Match 28.6%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
:||
Db 3 EDL 5

RESULT 11
PT0533
T-cell receptor beta chain V-D-J region (126-1AA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0533
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0533
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Cross-references: UNIPARC:UPI000017C801
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DD 5
||
Db 4 DD 5

RESULT 12
A34026
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C;Accession: A34026
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.;
J. Biol. Chem. 263, 1140-1145, 1988
A;Title: Divergence in primary structure between the molecular forms of acetylcholinest
A;Reference number: A34026; MUID:88087239; PMID:3335534
A;Accession: A34026
A;Molecule type: protein
A;Residues: 1-7 <GIB>
A;Cross-references: UNIPARC:UPI000017BF32
C;Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 LLEA 9
|| |
Db 1 LLNA 4

RESULT 13
B39040
calsequestrin, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
R;Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casei
A;Reference number: A39040; MUID:91093153; PMID:1985907
A;Accession: B39040
A;Status: preliminary
A;Molecule type: protein

A;Residues: 1-7 <CAL>
A;Cross-references: UNIPARC:UPI000017C5BC
C;Keywords: phosphoprotein; skeletal muscle

Query Match 28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 DD 5
              ||
Db          1 DD 2
```

RESULT 14
PT0628
T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0628
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Cross-references: UNIPARC:UPI000017C7CD
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 DD 5
              ||
Db          4 DD 5
```

RESULT 15
PT0722
T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0722
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0722
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-7 <FEE>
A;Cross-references: UNIPARC:UPI000017C81F
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 28.6%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 DD 5
              ||
Db          4 DD 5
```

Search completed: April 6, 2006, 16:26:10
Job time : 18.6667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:13:46 ; Search time 118 Seconds
(without alignments)
53.811 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	42.9	8	2	Q7XB03_MAIZE	Q7xb03 zea mays (m
2	18	42.9	9	2	Q7X8P7_MAIZE	Q7x8p7 zea mays (m
3	16	38.1	9	2	Q70SM2_HUMAN	Q70sm2 homo sapien
4	16	38.1	9	2	Q7KYP6_HUMAN	Q7kyp6 homo sapien
5	16	38.1	9	2	Q8LPT5_MAIZE	Q8lpt5 zea mays (m
6	16	38.1	9	2	P82568_STRPY	P82568 streptococc
7	15	35.7	8	2	P72279_RHOGO	P72279 rhodococcus
8	15	35.7	8	2	Q80H91_9PARA	Q80h91 newcastle d
9	15	35.7	9	2	Q9UE26_HUMAN	Q9ue26 homo sapien
10	15	35.7	9	2	Q9XJN0_9VIRU	Q9xjn0 bacteriopha
11	15	35.7	9	2	Q4QWV3_9MARC	Q4qwv3 pallavicini
12	15	35.7	9	2	Q4QWV9_9MARC	Q4qwv9 jensenia sp
13	15	35.7	9	2	P83539_LACSN	P83539 lactobacill
14	14	33.3	8	2	Q51594_9ZZZZ	Q51594 plasmid col
15	14	33.3	8	2	Q8KPX4_9CHRO	Q8kpx4 microcystis
16	14	33.3	8	2	Q9ZIE9_NEIME	Q9zie9 neisseria m
17	14	33.3	9	2	Q7M4R5_HUMAN	Q7m4r5 homo sapien
18	14	33.3	9	2	Q9FSZ2_CICAR	Q9fsz2 cicer ariet
19	14	33.3	9	2	Q563E0_9CYAN	Q563e0 uncultured
20	14	33.3	9	2	Q9QZA8_MOUSE	Q9qza8 mus musculu
21	14	33.3	9	2	Q6Q7G0_RANRI	Q6q7g0 rana ridibu
22	14	33.3	9	2	Q85710_9RETR	Q85710 rous sarcom
23	14	33.3	9	2	Q8UTD7_9HIV1	Q8utd7 human immun
24	13	31.0	7	2	Q15897_HUMAN	Q15897 homo sapien
25	13	31.0	8	2	Q9HDS4_ASPFL	Q9hds4 aspergillus
26	13	31.0	8	2	Q5RLS1_PIG	Q5rls1 sus scrofa
27	13	31.0	8	2	Q6JC68_SOYBN	Q6jc68 glycine max
28	13	31.0	8	2	Q93SR0_STAEP	Q93sr0 staphylococ
29	13	31.0	8	2	Q9QVJ8_9MURI	Q9qvj8 mus sp. mep
30	13	31.0	8	2	O89965_POVJC	O89965 polyomaviru
31	13	31.0	8	2	Q6PUD5_SV40	Q6pud5 simian viru
32	13	31.0	8	2	Q6PUD7_SV40	Q6pud7 simian viru
33	13	31.0	8	2	Q6PUD9_SV40	Q6pud9 simian viru
34	13	31.0	8	2	Q6PUE1_SV40	Q6pue1 simian viru
35	13	31.0	8	2	Q6QSX9_SV40	Q6qsx9 simian viru
36	13	31.0	8	2	Q64IX4_FUNHE	Q64ix4 fundulus he
37	13	31.0	9	1	IPYR_RHOVI	P82992 rhodopseudo
38	13	31.0	9	2	Q7RY89_NEUCR	Q7ry89 neurospora
39	13	31.0	9	2	Q6LCV2_HUMAN	Q6lcv2 homo sapien
40	13	31.0	9	2	Q6UVK2_MALDO	Q6uvk2 malus domes
41	13	31.0	9	2	Q56SS9_SAMCA	Q56ss9 sambucus ca
42	13	31.0	9	2	Q56ST0_9DIPS	Q56st0 viburnum ut
43	13	31.0	9	2	Q56ST1_9DIPS	Q56st1 viburnum ur
44	13	31.0	9	2	Q56ST2_9DIPS	Q56st2 viburnum tr
45	13	31.0	9	2	Q56ST3_VIBOP	Q56st3 viburnum op

ALIGNMENTS

RESULT 1
Q7XB03_MAIZE
ID Q7XB03_MAIZE PRELIMINARY; PRT; 8 AA.
AC Q7XB03;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Y-3;
RX MEDLINE=22779048; PubMed=12897253; DOI=10.1105/tpc.012526;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300612; AAP55351.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 915 MW; 5D1862CAB4072054 CRC64;

Query Match 42.9%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VLRD 4
              :|||
Db          2 ILRD 5
```

RESULT 2
Q7X8P7_MAIZE
ID Q7X8P7_MAIZE PRELIMINARY; PRT; 9 AA.
AC Q7X8P7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Y-13, and W-16;
RX MEDLINE=22779048; PubMed=12897253; DOI=10.1105/tpc.012526;

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RA   Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT   "Contrasting effects of selection on sequence diversity and linkage
RT   disequilibrium at two phytoene synthase loci.";
RL   Plant Cell 15:1795-1806(2003).
DR   EMBL; AY300641; AAP55379.1; -; Genomic_DNA.
DR   EMBL; AY300665; AAP55403.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1016 MW;  1D1C62CAB4072054 CRC64;

  Query Match             42.9%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRD 4
              :|||
Db          3 ILRD 6


RESULT 3
Q70SM2_HUMAN
ID   Q70SM2_HUMAN PRELIMINARY;      PRT;     9 AA.
AC   Q70SM2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypermethylated in cancer 1 (Fragment).
GN   Name=HIC1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RA   Pinte S., Guerardel C., Deltour S., Godwin A.K., Leprince D.;
RT   "Identification of a second G-C-rich promoter conserved in the human,
RT   murine and rat tumor suppressor genes HIC1.";
RL   Oncogene 23:4023-4031(2004).
DR   EMBL; AJ550616; CAD79467.1; -; mRNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  964 MW;  5B5E6DDB1681AAA7 CRC64;

  Query Match             38.1%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              | :||
Db          3 DTMEA 7


RESULT 4
Q7KYP6_HUMAN
ID   Q7KYP6_HUMAN PRELIMINARY;      PRT;     9 AA.
AC   Q7KYP6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Mi.V glycoprotein (exon P3B) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Miltenberger class V;
RX   MEDLINE=90005483; PubMed=2792104;
RA   Vignal A., Rahuel C., El-Maliki B., London J., Le Vankim C.,
RA   Blanchard C.D.;
RT   "Molecular Analysis of glycophorin A and B gene structure and
RT   expression . . . . .";
RL   Eur. J. Biochem. 184:337-344(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Miltenberger class V;
RA   Vignal A., Rahuel C., El-Maliki B., London J., Le Vankim C.,
RA   Blanchard C.D.;
RT   "Molecular Analysis of glycophorin A and B gene structure and
RT   expression . . . . .";
RL   Eur. J. Biochem. 184:0-0(1989).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Miltenberger class V;
RA   Cartron J.P.;
RL   Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X15824; CAA33822.1; -; Genomic_DNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1073 MW;  50D145B7244AB403 CRC64;

  Query Match             38.1%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDL 6
              ||:|
Db          3 RDNL 6


RESULT 5
Q8LPT5_MAIZE
ID   Q8LPT5_MAIZE PRELIMINARY;      PRT;     9 AA.
AC   Q8LPT5;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-expansin-like protein (Fragment).
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA   Morgante M., Rafalski J.A.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY094310; AAM21836.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  977 MW;  5C05B2D2CB1AAAA3 CRC64;

  Query Match             38.1%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLEA 9
              |::::|
Db          4 DEVVDA 9


RESULT 6
P82568_STRPY
ID   P82568_STRPY  PRELIMINARY;      PRT;     9 AA.
AC   P82568;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Unknown protein from 2D-page (Fragment).
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
```

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RC   STRAIN=JRS4;
RA   Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA   VanBogelen R.A.;
RT   "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT   proteins.";
RL   Submitted (MAY-2000) to Swiss-Prot.
CC   -!- MASS SPECTROMETRY: MW=22592.04; METHOD=Electrospray.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1069 MW;  2A771042CB1AB2D7 CRC64;

  Query Match             38.1%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              |:::|
Db          4 DEVIE 8


RESULT 7
P72279_RHOGO
ID   P72279_RHOGO PRELIMINARY;      PRT;     8 AA.
AC   P72279;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Biphenyl dioxygenase (Fragment).
GN   Name=bphB;
OS   Rhodococcus globerulus.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Nocardiaceae; Rhodococcus.
OX   NCBI_TaxID=33008;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95255652; PubMed=7737502; DOI=10.1016/0378-1119(94)00530-6;
RA   Asturias J.A., Diaz E., Timmis K.N.;
RT   "Evolutionary relationship of the biphenyl dioxygenase of the gram-
RT   positve bacterium Rhodococcus globerulus P6 to multicomponent
RT   dioxygenases of gram-negative bacteria.";
RL   Gene 156:11-18(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Asturias J.;
RL   Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X80041; CAA56350.1; -; Genomic_DNA.
DR   GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
KW   Dioxygenase.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  989 MW;  EBD2CB1AB6D73406 CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 8;
  Best Local Similarity   33.3%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLL 7
              |:|:::
Db          3 LQDEVV 8


RESULT 8
Q80H91_9PARA
ID   Q80H91_9PARA PRELIMINARY;      PRT;     8 AA.
AC   Q80H91;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   HN/HN0 (Fragment).
GN   Name=HN/HN0;
OS   Newcastle disease virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Avulavirus.
OX   NCBI_TaxID=11176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94175786; PubMed=8129624;
RA   Collins M.S., Strong I., Alexander D.J.;
RT   "Evaluation of the molecular basis of pathogenicity of the variant
RT   Newcastle disease viruses termed 'pigeon PMV-1 viruses'.";
RL   Arch. Virol. 134:403-411(1994).
DR   EMBL; S69419; AAP19628.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  929 MW;  33D4087AA337205B CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRD 4
              :|:|
Db          2 ILKD 5


RESULT 9
Q9UE26_HUMAN
ID   Q9UE26_HUMAN PRELIMINARY;      PRT;     9 AA.
AC   Q9UE26;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   PEG1/MEST protein.
GN   Name=PEG1/MEST;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97336048; PubMed=9192843; DOI=10.1006/geno.1997.4731;
RA   Riesewijk A.M., Hu L., Schulz U., Tariveridan G., Hoeglund P.,
RA   Kere J., Ropers H.H., Kalscheuer V.M.;
RT   "Monoallelic expression of human PEG1/MEST is paralleled by parent-
RT   specific methylation in fetuses.";
RL   Genomics 42:236-244(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalscheuer V.M.M.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y10620; CAA71631.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; NAS.
SQ   SEQUENCE   9 AA;  1258 MW;  C52D07340AB41412 CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+06;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 VLRDDL 6
              | || |
Db          2 VRRDRL 7


RESULT 10
Q9XJN0_9VIRU
ID   Q9XJN0_9VIRU PRELIMINARY;      PRT;     9 AA.
AC   Q9XJN0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   P10 (Fragment).
OS   Bacteriophage phi-10.
OC   Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
OX   NCBI_TaxID=90889;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99350412; PubMed=10419946;
```

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RA   Mindich L., Qiao X., Qiao J., Onodera S., Romantschuk M.,
RA   Hoogstraten D.;
RT   "Isolation of additional bacteriophages with genomes of segmented
RT   double-stranded RNA.";
RL   J. Bacteriol. 181:4505-4508(1999).
DR   EMBL; AF125675; AAD22555.1; -; Genomic_RNA.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1058 MW;  880E376AA720544A CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 2.2e+06;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              |::|:
Db          2 DNILD 6


RESULT 11
Q4QWV3_9MARC
ID   Q4QWV3_9MARC PRELIMINARY;      PRT;     9 AA.
AC   Q4QWV3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   AtpB (Fragment).
GN   Name=atpB;
OS   Pallavicinia rubristipa.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC   Jungermanniopsida; Metzgeriidae; Metzgeriales; Pallaviciniineae;
OC   Pallaviciniaceae; Pallavicinia.
OX   NCBI_TaxID=280539;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Forrest L.L., Schuette S.W., Crandall-Stotler B.J., Stotler R.E.;
RT   "A Molecular Study of the Simple Thalloid Liverwort Jensenia
RT   (Marchantiophyta, Pallaviciniaceae).";
RL   Bryologist 108:204-211(2005).
DR   EMBL; AY734732; AAX46221.1; -; Genomic_DNA.
KW   Chloroplast.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1030 MW;  6D4E2727272451B4 CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LRDDLL 7
              :| :||
Db          1 MRTNLL 6


RESULT 12
Q4QWV9_9MARC
ID   Q4QWV9_9MARC PRELIMINARY;      PRT;     9 AA.
AC   Q4QWV9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   AtpB (Fragment).
GN   Name=atpB;
OS   Jensenia spinosa.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC   Jungermanniopsida; Metzgeriidae; Metzgeriales; Pallaviciniineae;
OC   Pallaviciniaceae; Jensenia.
OX   NCBI_TaxID=280534;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Forrest L.L., Schuette S.W., Crandall-Stotler B.J., Stotler R.E.;
RT   "A Molecular Study of the Simple Thalloid Liverwort Jensenia
RT   (Marchantiophyta, Pallaviciniaceae).";
RL   Bryologist 108:204-211(2005).
DR   EMBL; AY734726; AAX46211.1; -; Genomic_DNA.
KW   Chloroplast.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1030 MW;  6D4E2727272451B4 CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LRDDLL 7
              :| :||
Db          1 MRTNLL 6


RESULT 13
P83539_LACSN
ID   P83539_LACSN PRELIMINARY;      PRT;     9 AA.
AC   P83539;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Unknown protein from 2D-page (Fragment).
OS   Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC   Lactobacillus.
OX   NCBI_TaxID=1625;
RN   [1]
RP   PROTEIN SEQUENCE, AND INDUCTION.
RC   STRAIN=DSM 20451;
RX   PubMed=12112860;
RX   DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
RA   Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT   "High pressure effects step-wise altered protein expression in
RT   Lactobacillus sanfranciscensis.";
RL   Proteomics 2:765-774(2002).
CC   -!- INDUCTION: By elevated hydrostatic pressure.
CC   -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC       protein is: 65 kDa.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1099 MW;  707B2455B72AA734 CRC64;

  Query Match             35.7%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+06;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 LRDDL 6
              || ||
Db          1 LRLDL 5


RESULT 14
Q51594_9ZZZZ
ID   Q51594_9ZZZZ PRELIMINARY;      PRT;     8 AA.
AC   Q51594;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CopB protein (Fragment).
OS   Plasmid ColV2-K94.
OG   Plasmid ColV2-K94.
OC   other sequences; plasmids.
OX   NCBI_TaxID=2458;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86223772; PubMed=2423502;
RA   Weber P.C., Palchaudhuri S.;
RT   "Incompatibility repressor in a RepA-like replicon of the IncFI
RT   plasmid ColV2-K94.";
RL   J. Bacteriol. 166:1106-1112(1986).
DR   EMBL; M13472; AAA23194.1; -; Genomic_DNA.
KW   Plasmid.
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FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  998 MW;  0F37205AA73416D7 CRC64;

  Query Match             33.3%;  Score 14;  DB 2;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |:|:
Db          3 RLDILK 8


RESULT 15
Q8KPX4_9CHRO
ID   Q8KPX4_9CHRO PRELIMINARY;      PRT;     8 AA.
AC   Q8KPX4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Phycocyanin alpha subunit (Fragment).
GN   Name=pcA;
OS   Microcystis sp. T96-1.
OC   Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX   NCBI_TaxID=198099;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22338268; PubMed=12450830;
RX   DOI=10.1128/AEM.68.12.6070-6076.2002;
RA   Baker J.A., Entsch B., Neilan B.A., McKay D.B.;
RT   "Monitoring changing toxigenicity of a cyanobacterial bloom by
RT   molecular methods.";
RL   Appl. Environ. Microbiol. 68:6070-6076(2002).
DR   EMBL; AY117046; AAM54719.1; -; Genomic_DNA.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  890 MW;  F4DB01A73771A336 CRC64;

  Query Match             33.3%;  Score 14;  DB 2;  Length 8;
  Best Local Similarity   37.5%;  Pred. No. 2.2e+06;
  Matches    3;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 LRDDLLEA 9
              ::  | ||
Db          1 MKTPLTEA 8


Search completed: April  6, 2006, 16:25:10
Job time : 120 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:25:31 ; Search time 27.3333 Seconds
(without alignments)
27.222 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	2	US-09-269-250E-18	Sequence 18, Appl
2	42	100.0	9	2	US-09-489-760-5	Sequence 5, Appli
3	37	88.1	9	2	US-09-269-250E-20	Sequence 20, Appl
4	37	88.1	9	2	US-09-489-760-2	Sequence 2, Appli
5	36	85.7	9	2	US-09-269-250E-29	Sequence 29, Appl
6	36	85.7	9	2	US-09-489-760-1	Sequence 1, Appli
7	27	64.3	9	2	US-09-217-609A-11	Sequence 11, Appl
8	27	64.3	9	2	US-08-873-235B-11	Sequence 11, Appl
9	23	54.8	8	2	US-09-269-250E-38	Sequence 38, Appl
10	22	52.4	7	2	US-08-556-419-14	Sequence 14, Appl
11	22	52.4	9	2	US-09-489-760-4	Sequence 4, Appli
12	21	50.0	6	1	US-08-459-568-20	Sequence 20, Appl
13	21	50.0	6	1	US-08-399-411-20	Sequence 20, Appl
14	21	50.0	6	2	US-08-516-859A-20	Sequence 20, Appl
15	21	50.0	6	2	US-09-586-472-20	Sequence 20, Appl
16	21	50.0	6	2	US-09-528-706-20	Sequence 20, Appl
17	21	50.0	7	2	US-10-122-675-6	Sequence 6, Appli
18	21	50.0	8	1	US-08-459-568-75	Sequence 75, Appl
19	21	50.0	8	1	US-08-399-411-75	Sequence 75, Appl
20	21	50.0	8	1	US-08-539-432-1	Sequence 1, Appli
21	21	50.0	8	2	US-08-516-859A-75	Sequence 75, Appl
22	21	50.0	8	2	US-09-586-472-75	Sequence 75, Appl
23	21	50.0	8	2	US-09-528-706-75	Sequence 75, Appl
24	21	50.0	8	2	US-08-453-485E-13	Sequence 13, Appl
25	21	50.0	9	1	US-08-459-568-72	Sequence 72, Appl
26	21	50.0	9	1	US-08-459-568-78	Sequence 78, Appl
27	21	50.0	9	1	US-08-399-411-72	Sequence 72, Appl
28	21	50.0	9	1	US-08-399-411-78	Sequence 78, Appl
29	21	50.0	9	2	US-08-516-859A-72	Sequence 72, Appl
30	21	50.0	9	2	US-08-516-859A-78	Sequence 78, Appl
31	21	50.0	9	2	US-09-586-472-72	Sequence 72, Appl
32	21	50.0	9	2	US-09-586-472-78	Sequence 78, Appl
33	21	50.0	9	2	US-09-528-706-72	Sequence 72, Appl
34	21	50.0	9	2	US-09-528-706-78	Sequence 78, Appl
35	21	50.0	9	2	US-09-744-549-15	Sequence 15, Appl
36	21	50.0	9	2	US-09-935-430-219	Sequence 219, App
37	21	50.0	9	2	US-09-935-430-565	Sequence 565, App
38	21	50.0	9	2	US-10-394-980-421	Sequence 421, App
39	21	50.0	9	2	US-10-394-980-464	Sequence 464, App
40	20	47.6	6	2	US-09-025-819-11	Sequence 11, Appl
41	20	47.6	6	2	US-09-808-126-11	Sequence 11, Appl
42	20	47.6	6	2	US-09-803-951-11	Sequence 11, Appl
43	20	47.6	8	2	US-08-747-599A-47	Sequence 47, Appl
44	20	47.6	8	2	US-08-747-599A-50	Sequence 50, Appl
45	20	47.6	8	2	US-08-747-599A-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-269-250E-18
; Sequence 18, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-18

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-09-489-760-5
; Sequence 5, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: KIAA0223 partial complementary DNA

US-09-489-760-5

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
||||||||| |
Db 1 VLRDDLLEA 9

RESULT 3
US-09-269-250E-20
; Sequence 20, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-09-269-250E-20

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| |||||| |
Db 1 VLHDDLLEA 9

RESULT 4
US-09-489-760-2
; Sequence 2, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
US-09-489-760-2

Query Match 88.1%; Score 37; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| |||||| |
Db 1 VLHDDLLEA 9

RESULT 5

US-09-269-250E-29
; Sequence 29, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa
; TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
; FILE REFERENCE: 58994
; CURRENT APPLICATION NUMBER: US/09/269,250E
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-09-269-250E-29

Query Match 85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| |||||| |
Db 1 VLXDDLLEA 9

RESULT 6
US-09-489-760-1
; Sequence 1, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
; APPLICANT: Rijksuniversiteit Te Leidin
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Hard, Victor H
; TITLE OF INVENTION: The HA-1 Antigen
; FILE REFERENCE: 2183-4285US
; CURRENT APPLICATION NUMBER: US/09/489,760
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: PCT/NL98/00424
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Histocompatibility antigen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (3)
; OTHER INFORMATION: AMINO ACID X REPRESENTS A HISTIDINE OR AN ARGININE
; OTHER INFORMATION: RESIDUE
US-09-489-760-1

Query Match 85.7%; Score 36; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|| |||||| |
Db 1 VLXDDLLEA 9

RESULT 7
US-09-217-609A-11
; Sequence 11, Application US/09217609A
; Patent No. 6071733
; GENERAL INFORMATION:
; APPLICANT: MURAMATSU, Masayoshi

```
;    APPLICANT:  KOIKE, Ayumi
;    APPLICANT:  OGURA, Kyozo
;    APPLICANT:  KOYAMA, Tanetoshi
;    APPLICANT:  SHIMIZU, Naoto
;    APPLICANT:  CHO, Yenwin
;    TITLE OF INVENTION:  Prenyl Diphosphate Synthetase Genes
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, NW - Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/217,609A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/873,235
;      FILING DATE:  11-Jun-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TOFFENETTI, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  10235/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-217-609A-11

  Query Match             64.3%;  Score 27;  DB 2;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLLE 8
              :|||:|:
Db          3 IRDDILD 9


RESULT 8
US-08-873-235B-11
; Sequence 11, Application US/08873235B
; Patent No. 6174715
;  GENERAL INFORMATION:
;    APPLICANT:  MURAMATSU, Masayoshi
;    APPLICANT:  KOIKE, Ayumi
;    APPLICANT:  OGURA, Kyozo
;    APPLICANT:  KOYAMA, Tanetoshi
;    APPLICANT:  SHIMIZU, Naoto
;    APPLICANT:  CHO, Yenwin
;    TITLE OF INVENTION:  Prenyl Diphosphate Synthetase Genes
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenyon & Kenyon
;      STREET:  1025 Connecticut Avenue, NW - Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1 for Windows
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/873,235B
;      FILING DATE:  11-Jun-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 154441/1996
;      FILING DATE:  14-Jun-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TOFFENETTI, Judith L.
;      REGISTRATION NUMBER:  39,048
;      REFERENCE/DOCKET NUMBER:  10235/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-429-1776
;      TELEFAX:  202-429-0796
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-873-235B-11

  Query Match             64.3%;  Score 27;  DB 2;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLLE 8
              :|||:|:
Db          3 IRDDILD 9


RESULT 9
US-09-269-250E-38
; Sequence 38, Application US/09269250E
; Patent No. 6830883
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 58994
;  CURRENT APPLICATION NUMBER: US/09/269,250E
;  CURRENT FILING DATE:  1999-05-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HUMAN
US-09-269-250E-38

  Query Match             54.8%;  Score 23;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 DLLEA 9
              |||||
Db          4 DLLEA 8


RESULT 10
US-08-556-419-14
; Sequence 14, Application US/08556419C
; Patent No. 6093549
; GENERAL INFORMATION:
;  APPLICANT: Ross, Christopher
;  APPLICANT: Li, Xiao-Jiang
;  APPLICANT: Li, Shi-Hua
;  APPLICANT: Sharp, Alan
;  APPLICANT: Lanahan, Anthony
;  APPLICANT: Worley, Paul
;  APPLICANT: Snyder, Solomon
;  TITLE OF INVENTION: Huntingtin-associated protein
```

```
;  FILE REFERENCE: 01107.52271
;  CURRENT APPLICATION NUMBER: US/08/556,419C
;  CURRENT FILING DATE: 1995-11-09
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;    LENGTH: 7
;    TYPE: PRT
;    ORGANISM: Rattus norvegicus
US-08-556-419-14

  Query Match             52.4%;  Score 22;  DB 2;  Length 7;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||||:
Db          1 DDLLQ 5


RESULT 11
US-09-489-760-4
; Sequence 4, Application US/09489760
; Patent No. 6878375
; GENERAL INFORMATION:
;  APPLICANT: Rijksuniversiteit Te Leidin
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT: Hunt, Donald F
;  APPLICANT: Hard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/09/489,760
;  CURRENT FILING DATE: 2000-01-21
;  EARLIER APPLICATION NUMBER: PCT/NL98/00424
;  EARLIER FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;    LENGTH: 9
;    TYPE: PRT
;    ORGANISM: Histocompatibility antigen
;    FEATURE:
;    NAME/KEY: PEPTIDE
;    LOCATION: (2)..(7)
;    OTHER INFORMATION: AMINO ACIDS X REPRESENT LEUCINE OR ISOLEUCINE
;    OTHER INFORMATION: RESIDUES
US-09-489-760-4

  Query Match             52.4%;  Score 22;  DB 2;  Length 9;
  Best Local Similarity   55.6%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |  ||  ||
Db          1 VXHDDXXEA 9


RESULT 12
US-08-459-568-20
; Sequence 20, Application US/08459568
; Patent No. 5811304
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/459,568
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-459-568-20

  Query Match             50.0%;  Score 21;  DB 1;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 4.6e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5


RESULT 13
US-08-399-411-20
; Sequence 20, Application US/08399411
; Patent No. 5831008
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  93
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell and Flores
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/399,411
;      FILING DATE:  06-MAR-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1264
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-399-411-20
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Query Match 50.0%; Score 21; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5
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RESULT 14
US-08-516-859A-20
; Sequence 20, Application US/08516859A
; Patent No. 6069231
;  GENERAL INFORMATION:
;    APPLICANT:  Huang, Shi
;    TITLE OF INVENTION:  Retinoblastoma Protein - Interacting
;    TITLE OF INVENTION:  Zinc Finger Proteins
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/516,859A
;      FILING DATE:  18-AUG-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/399,411
;      FILING DATE:  06-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/292,683
;      FILING DATE:  18-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 1776
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-516-859A-20
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Query Match 50.0%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5
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RESULT 15
US-09-586-472-20
; Sequence 20, Application US/09586472
; Patent No. 6323335
;   GENERAL INFORMATION:
;        APPLICANT: Huang, Shi
;        TITLE OF INVENTION: Retinoblastoma Protein - Interacting
;                            Zinc Finger Proteins
;        NUMBER OF SEQUENCES: 106
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Campbell & Flores LLP
;             STREET: 4370 La Jolla Village Drive, Suite 700
;             CITY: San Diego
;             STATE: California
;             COUNTRY: USA
;             ZIP: 92122
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/586,472
;             FILING DATE: 01-Jun-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/528,706
;             FILING DATE: 17-MAR-2000
;             APPLICATION NUMBER: US 08/516,859
;             FILING DATE: 18-AUG-1995
;             APPLICATION NUMBER: US 08/399,411
;             FILING DATE: 06-MAR-1995
;             APPLICATION NUMBER: US 08/292,683
;             FILING DATE: 18-AUG-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Campbell, Cathryn A.
;             REGISTRATION NUMBER: 31,815
;             REFERENCE/DOCKET NUMBER: P-LJ 4130
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (619) 535-9001
;             TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 6 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-586-472-20
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Query Match 50.0%; Score 21; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          4 DDLLE 8
              :||||
Db          1 EDLLE 5
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Search completed: April 6, 2006, 16:27:37
Job time : 27.6667 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:44:31 ; Search time 90.3333 Seconds
(without alignments)
41.629 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	4	US-10-623-176-10	Sequence 10, Appl
2	42	100.0	9	4	US-10-791-217-5	Sequence 5, Appli
3	42	100.0	9	6	US-11-007-740-18	Sequence 18, Appl
4	38	90.5	9	4	US-10-623-176-42	Sequence 42, Appl
5	38	90.5	9	4	US-10-623-176-46	Sequence 46, Appl
6	37	88.1	9	4	US-10-623-176-2	Sequence 2, Appli
7	37	88.1	9	4	US-10-791-217-2	Sequence 2, Appli
8	37	88.1	9	5	US-10-861-335-1	Sequence 1, Appli
9	37	88.1	9	6	US-11-007-740-20	Sequence 20, Appl
10	36	85.7	9	4	US-10-623-176-1	Sequence 1, Appli
11	36	85.7	9	4	US-10-791-217-1	Sequence 1, Appli
12	36	85.7	9	6	US-11-007-740-29	Sequence 29, Appl
13	34	81.0	9	4	US-10-623-176-48	Sequence 48, Appl
14	33	78.6	9	4	US-10-623-176-23	Sequence 23, Appl
15	33	78.6	9	4	US-10-623-176-41	Sequence 41, Appl
16	33	78.6	9	4	US-10-623-176-45	Sequence 45, Appl
17	29	69.0	9	4	US-10-623-176-5	Sequence 5, Appli
18	29	69.0	9	4	US-10-623-176-47	Sequence 47, Appl
19	28	66.7	9	4	US-10-623-176-40	Sequence 40, Appl
20	25	59.5	9	3	US-09-834-765-349	Sequence 349, App
21	25	59.5	9	4	US-10-623-176-39	Sequence 39, Appl
22	24	57.1	7	4	US-10-271-708-16	Sequence 16, Appl
23	24	57.1	9	4	US-10-623-176-4	Sequence 4, Appli
24	24	57.1	9	5	US-10-503-135-26	Sequence 26, Appl
25	24	57.1	9	5	US-10-503-135-64	Sequence 64, Appl
26	23	54.8	8	4	US-10-623-176-15	Sequence 15, Appl
27	23	54.8	8	6	US-11-007-740-38	Sequence 38, Appl
28	23	54.8	9	3	US-09-834-765-132	Sequence 132, App
29	23	54.8	9	4	US-10-623-176-3	Sequence 3, Appli
30	22	52.4	9	4	US-10-623-176-14	Sequence 14, Appl
31	22	52.4	9	4	US-10-791-217-4	Sequence 4, Appli
32	22	52.4	9	6	US-11-007-740-40	Sequence 40, Appl
33	21	50.0	7	3	US-09-990-186-208	Sequence 208, App
34	21	50.0	7	3	US-09-990-186-211	Sequence 211, App
35	21	50.0	7	3	US-09-990-186-216	Sequence 216, App
36	21	50.0	7	3	US-09-989-994-208	Sequence 208, App
37	21	50.0	7	3	US-09-989-994-211	Sequence 211, App
38	21	50.0	7	3	US-09-989-994-216	Sequence 216, App
39	21	50.0	7	4	US-10-122-675-6	Sequence 6, Appli
40	21	50.0	7	5	US-10-487-268-9	Sequence 9, Appli
41	21	50.0	8	4	US-10-700-330-169	Sequence 169, App
42	21	50.0	9	3	US-09-935-430-219	Sequence 219, App
43	21	50.0	9	3	US-09-935-430-565	Sequence 565, App
44	21	50.0	9	3	US-09-833-203-54	Sequence 54, Appl
45	21	50.0	9	4	US-10-119-536A-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-10-623-176-10
; Sequence 10, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-1 epitopes and uses thereof
; FILE REFERENCE: 2183-6047US
; CURRENT APPLICATION NUMBER: US/10/623,176
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/489,760
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: EP 97202303.0
; PRIOR FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: PCT/NL98/00424
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 2000-504165
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(9)
US-10-623-176-10

Query Match 100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
||||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-10-791-217-5
; Sequence 5, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Elsa A.J.M
; APPLICANT: Hunt, Donald F
; APPLICANT: Engelhard, Victor H

```
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from KIAA0223 partial complementary DNA
US-10-791-217-5

  Query Match             100.0%;  Score 42;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 3
US-11-007-740-18
; Sequence 18, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-18

  Query Match             100.0%;  Score 42;  DB 6;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              |||||||||
Db          1 VLRDDLLEA 9


RESULT 4
US-10-623-176-42
; Sequence 42, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-42

  Query Match             90.5%;  Score 38;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              ||||||||
Db          2 VLRDDLLE 9


RESULT 5
US-10-623-176-46
; Sequence 46, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-46

  Query Match             90.5%;  Score 38;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LRDDLLEA 9
              ||||||||
Db          1 LRDDLLEA 8


RESULT 6
US-10-623-176-2
; Sequence 2, Application US/10623176
; Publication No. US20040092446A1
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; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-2

  Query Match             88.1%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 7
US-10-791-217-2
; Sequence 2, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
US-10-791-217-2

  Query Match             88.1%;  Score 37;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 8
US-10-861-335-1
; Sequence 1, Application US/10861335
; Publication No. US20050031612A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M.
;  TITLE OF INVENTION: Minor histocompatibility antigen HA-1: target antigen for immunc
;  TITLE OF INVENTION:  of tumors
;  FILE REFERENCE: 2183-6479US
;  CURRENT APPLICATION NUMBER: US/10/861,335
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: PCT/NL02/00791
;  PRIOR FILING DATE: 2002-12-05
;  PRIOR APPLICATION NUMBER: EP 01204704.9
;  PRIOR FILING DATE: 2001-12-05
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HA-1 peptide
US-10-861-335-1

  Query Match             88.1%;  Score 37;  DB 5;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 9
US-11-007-740-20
; Sequence 20, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon Fragments
US-11-007-740-20

  Query Match             88.1%;  Score 37;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLHDDLLEA 9


RESULT 10
US-10-623-176-1
; Sequence 1, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
```

```
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   OTHER INFORMATION: wherein X can be R or H
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-1

  Query Match             85.7%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 11
US-10-791-217-1
; Sequence 1, Application US/10791217
; Publication No. US20040191268A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa A.J.M
;  APPLICANT:  Hunt, Donald F
;  APPLICANT:  Engelhard, Victor H
;  TITLE OF INVENTION: The HA-1 Antigen
;  FILE REFERENCE: 2183-4285US
;  CURRENT APPLICATION NUMBER: US/10/791,217
;  CURRENT FILING DATE:  2004-03-02
;  PRIOR APPLICATION NUMBER: US/09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: obtained from histocompatibility antigen
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa is HISTIDINE OR ARGININE RESIDUE
US-10-791-217-1

  Query Match             85.7%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 12
US-11-007-740-29
; Sequence 29, Application US/11007740
; Publication No. US20050233350A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Elsa
;  TITLE OF INVENTION: METHOD FOR TYPING OF MINOR HISTOCOMPATIBILITY ANTIGEN HA-1
;  FILE REFERENCE: 2799/58994-A
;  CURRENT APPLICATION NUMBER: US/11/007,740
;  CURRENT FILING DATE:  2004-12-08
;  PRIOR APPLICATION NUMBER: 09/269,250
;  PRIOR FILING DATE: 1999-05-21
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa represents a histidine (H) or an arginine (R) residue
US-11-007-740-29

  Query Match             85.7%;  Score 36;  DB 6;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.7e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || ||||||
Db          1 VLXDDLLEA 9


RESULT 13
US-10-623-176-48
; Sequence 48, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-48

  Query Match             81.0%;  Score 34;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDLLEA 9
              |||||||
```

```
Db          1 RDDLLEA 7


RESULT 14
US-10-623-176-23
; Sequence 23, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-23

  Query Match             78.6%;  Score 33;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VLRDDLL 7
              |||||||
Db          3 VLRDDLL 9


RESULT 15
US-10-623-176-41
; Sequence 41, Application US/10623176
; Publication No. US20040092446A1
; GENERAL INFORMATION:
;  APPLICANT: Goulmy, Els A.J.M.
;  APPLICANT:  Hunt, Donald F.
;  APPLICANT:  Engelhard, Victor H.
;  TITLE OF INVENTION: HA-1 epitopes and uses thereof
;  FILE REFERENCE: 2183-6047US
;  CURRENT APPLICATION NUMBER: US/10/623,176
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: 09/489,760
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: EP 97202303.0
;  PRIOR FILING DATE: 1997-07-23
;  PRIOR APPLICATION NUMBER: PCT/NL98/00424
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 2000-504165
;  PRIOR FILING DATE: 2000-01-24
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: HA-1 peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)..(9)
US-10-623-176-41

  Query Match             78.6%;  Score 33;  DB 4;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              || |||||
Db          2 VLHDDLLE 9


Search completed: April  6, 2006, 16:50:29
Job time : 90.3333 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 16:46:11 ; Search time 12.3333 Seconds
(without alignments)
22.762 Million cell updates/sec

Title: US-10-791-217A-5
Perfect score: 42
Sequence: 1 VLRDDLLEA 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 38721

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	100.0	9	7	US-11-010-748A-12	Sequence 12, Appl
2	37	88.1	9	7	US-11-010-748A-11	Sequence 11, Appl
3	21	50.0	4	7	US-11-019-027-17	Sequence 17, Appl
4	21	50.0	7	7	US-11-096-706-52	Sequence 52, Appl
5	21	50.0	7	7	US-11-225-686-208	Sequence 208, App
6	21	50.0	7	7	US-11-225-686-211	Sequence 211, App
7	21	50.0	7	7	US-11-225-686-216	Sequence 216, App
8	21	50.0	7	7	US-11-202-009-208	Sequence 208, App
9	21	50.0	7	7	US-11-202-009-211	Sequence 211, App
10	21	50.0	7	7	US-11-202-009-216	Sequence 216, App
11	21	50.0	9	6	US-10-989-767A-219	Sequence 219, App
12	21	50.0	9	6	US-10-989-767A-565	Sequence 565, App
13	20	47.6	5	7	US-11-129-143-168	Sequence 168, App
14	20	47.6	5	7	US-11-129-143-169	Sequence 169, App
15	20	47.6	5	7	US-11-129-143-170	Sequence 170, App
16	20	47.6	5	7	US-11-129-143-171	Sequence 171, App
17	20	47.6	5	7	US-11-129-143-172	Sequence 172, App
18	20	47.6	5	7	US-11-129-143-173	Sequence 173, App
19	20	47.6	7	6	US-10-982-440-126	Sequence 126, App
20	20	47.6	7	7	US-11-096-706-88	Sequence 88, Appl
21	20	47.6	7	7	US-11-096-706-164	Sequence 164, App
22	20	47.6	8	7	US-11-021-305-62	Sequence 62, Appl
23	20	47.6	8	7	US-11-021-305-65	Sequence 65, Appl
24	20	47.6	8	7	US-11-021-305-66	Sequence 66, Appl
25	20	47.6	9	6	US-10-927-435-63	Sequence 63, Appl
26	20	47.6	9	6	US-10-927-634-63	Sequence 63, Appl
27	19	45.2	7	7	US-11-225-686-2954	Sequence 2954, Ap
28	19	45.2	7	7	US-11-225-686-3877	Sequence 3877, Ap
29	19	45.2	7	7	US-11-225-686-3914	Sequence 3914, Ap
30	19	45.2	7	7	US-11-225-686-3915	Sequence 3915, Ap
31	19	45.2	7	7	US-11-225-686-3916	Sequence 3916, Ap
32	19	45.2	7	7	US-11-225-686-3932	Sequence 3932, Ap
33	19	45.2	7	7	US-11-225-686-3941	Sequence 3941, Ap
34	19	45.2	7	7	US-11-202-009-2954	Sequence 2954, Ap
35	19	45.2	7	7	US-11-202-009-3877	Sequence 3877, Ap
36	19	45.2	7	7	US-11-202-009-3914	Sequence 3914, Ap
37	19	45.2	7	7	US-11-202-009-3915	Sequence 3915, Ap
38	19	45.2	7	7	US-11-202-009-3916	Sequence 3916, Ap
39	19	45.2	7	7	US-11-202-009-3932	Sequence 3932, Ap
40	19	45.2	7	7	US-11-202-009-3941	Sequence 3941, Ap
41	19	45.2	8	7	US-11-045-024-575	Sequence 575, App
42	19	45.2	8	7	US-11-045-024-3138	Sequence 3138, Ap
43	19	45.2	8	7	US-11-045-024-3698	Sequence 3698, Ap
44	19	45.2	8	7	US-11-045-024-5495	Sequence 5495, Ap
45	19	45.2	8	7	US-11-045-024-5716	Sequence 5716, Ap

ALIGNMENTS

RESULT 1
US-11-010-748A-12
; Sequence 12, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T
; OTHER INFORMATION: ell epitopes
US-11-010-748A-12

Query Match 100.0%; Score 42; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLRDDLLEA 9
|||||||||
Db 1 VLRDDLLEA 9

RESULT 2
US-11-010-748A-11
; Sequence 11, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard

```
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
;  FILE REFERENCE: MER-136
;  CURRENT APPLICATION NUMBER: US/11/010,748A
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/EP03/06251
;  PRIOR FILING DATE: 2003-06-13
;  PRIOR APPLICATION NUMBER: EP02013423.5
;  PRIOR FILING DATE: 2002-06-13
;  NUMBER OF SEQ ID NOS: 926
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(9)
;   OTHER INFORMATION: Human minor histocompatibility antigens HA-1 characterized by T c
;   OTHER INFORMATION: ell epitopes
US-11-010-748A-11

  Query Match             88.1%;  Score 37;  DB 7;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLEA 9
              || |||||
Db          1 VLHDDLLEA 9


RESULT 3
US-11-019-027-17
; Sequence 17, Application US/11019027
; Publication No. US20050282181A1
; GENERAL INFORMATION:
;  APPLICANT: YAN, Wei
;  APPLICANT:  SHEN, Wenyan
;  APPLICANT:  ZHOU, Hongxing
;  APPLICANT:  ZHOU, Chen
;  APPLICANT:  COSMAN, David J.
;  APPLICANT:  CARTER, Paul
;  APPLICANT:  MARTIN, Francis H.
;  TITLE OF INVENTION: METHODS OF IDENTIFYING FUNCTIONAL ANTIBODIES
;  FILE REFERENCE: A-890A
;  CURRENT APPLICATION NUMBER: US/11/019,027
;  CURRENT FILING DATE:  2004-12-21
;  PRIOR APPLICATION NUMBER: 60/605,902
;  PRIOR FILING DATE: 2004-08-31
;  PRIOR APPLICATION NUMBER: 60/531,714
;  PRIOR FILING DATE: 2003-12-22
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 4
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: ER localization signal
US-11-019-027-17

  Query Match             50.0%;  Score 21;  DB 7;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDL 6
              ||||
Db          1 RDDL 4


RESULT 4
US-11-096-706-52
; Sequence 52, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
;  APPLICANT: Sangamo Biosciences, Inc.
;  APPLICANT:  Collingwood, Trevor
;  TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
;  FILE REFERENCE: 019496-008220US
;  CURRENT APPLICATION NUMBER: US/11/096,706
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 60/560,535
;  PRIOR FILING DATE: 2004-04-08
;  PRIOR APPLICATION NUMBER: US 60/576,757
;  PRIOR FILING DATE: 2004-06-02
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
;   OTHER INFORMATION: region)
US-11-096-706-52

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RDDL 6
              ||||
Db          2 RDDL 5


RESULT 5
US-11-225-686-208
; Sequence 208, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/225,686
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: US/09/989,994
;  PRIOR FILING DATE: 2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-208

  Query Match             50.0%;  Score 21;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 RDDLLE 8
              | |||:
Db          1 RSDLLQ 6


RESULT 6
US-11-225-686-211
; Sequence 211, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/11/225,686
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; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-211

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RDDLLE 8
| |||:
Db 1 RSDLLQ 6

RESULT 7
US-11-225-686-216
; Sequence 216, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-225-686-216

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RDDLLE 8
| |||:
Db 1 RSDLLQ 6

RESULT 8
US-11-202-009-208
; Sequence 208, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-208

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RDDLLE 8
| |||:
Db 1 RSDLLQ 6

RESULT 9
US-11-202-009-211
; Sequence 211, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-211

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RDDLLE 8
| |||:
Db 1 RSDLLQ 6

RESULT 10
US-11-202-009-216
; Sequence 216, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-11-202-009-216

Query Match 50.0%; Score 21; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RDDLLE 8

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              | |||:
Db          1 RSDLLQ 6


RESULT 11
US-10-989-767A-219
; Sequence 219, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
;  APPLICANT: FARIS, MARY
;  APPLICANT:  HUBERT, RENE
;  APPLICANT:  RAITANO, ARTHUR
;  APPLICANT:  AFAR, DANIEL
;  APPLICANT:  LEVIN, ELANA
;  APPLICANT:  CHALLITA-EID, PIA
;  APPLICANT:  JAKOBOVITZ, AYA
;  TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
;  TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
;  TITLE OF INVENTION:  OTHER CANCERS
;  FILE REFERENCE: 511582005004
;  CURRENT APPLICATION NUMBER: US/10/989,767A
;  CURRENT FILING DATE:  2004-11-15
;  PRIOR APPLICATION NUMBER: 10/277,292
;  PRIOR FILING DATE: 2002-10-21
;  PRIOR APPLICATION NUMBER: 09/935,430
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/227,098
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 60/282,739
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 700
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 219
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-219

  Query Match             50.0%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   37.5%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              ::: ||:|
Db          1 LMKSDLVE 8


RESULT 12
US-10-989-767A-565
; Sequence 565, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
;  APPLICANT: FARIS, MARY
;  APPLICANT:  HUBERT, RENE
;  APPLICANT:  RAITANO, ARTHUR
;  APPLICANT:  AFAR, DANIEL
;  APPLICANT:  LEVIN, ELANA
;  APPLICANT:  CHALLITA-EID, PIA
;  APPLICANT:  JAKOBOVITZ, AYA
;  TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
;  TITLE OF INVENTION:  USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
;  TITLE OF INVENTION:  OTHER CANCERS
;  FILE REFERENCE: 511582005004
;  CURRENT APPLICATION NUMBER: US/10/989,767A
;  CURRENT FILING DATE:  2004-11-15
;  PRIOR APPLICATION NUMBER: 10/277,292
;  PRIOR FILING DATE: 2002-10-21
;  PRIOR APPLICATION NUMBER: 09/935,430
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/227,098
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 60/282,739
;  PRIOR FILING DATE: 2001-04-10
;  NUMBER OF SEQ ID NOS: 700
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 565
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chemically synthesized peptide motif
US-10-989-767A-565

  Query Match             50.0%;  Score 21;  DB 6;  Length 9;
  Best Local Similarity   37.5%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VLRDDLLE 8
              ::: ||:|
Db          1 LMKSDLVE 8


RESULT 13
US-11-129-143-168
; Sequence 168, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Bradyrhizobium japonicum
US-11-129-143-168

  Query Match             47.6%;  Score 20;  DB 7;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DDLLE 8
              ||:|:
Db          1 DDILD 5


RESULT 14
US-11-129-143-169
; Sequence 169, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
;  APPLICANT: BERRY, Alan
;  APPLICANT:  BRETZEL, Werner
;  APPLICANT:  HUMBELIN, Markus
;  APPLICANT:  LOPEZ-ULIBARRI, Rual
;  APPLICANT:  MAYER, Anne F.
;  APPLICANT:  YELISEEV, Alexei A.
;  TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
;  FILE REFERENCE: C38435/121966
;  CURRENT APPLICATION NUMBER: US/11/129,143
;  CURRENT FILING DATE:  2005-05-13
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
;   LENGTH: 5
;   TYPE: PRT
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; ORGANISM: Rhizobium sp. strain NGR234
US-11-129-143-169

  Query Match 47.6%; Score 20; DB 7; Length 5;
  Best Local Similarity 60.0%; Pred. No. 1.4e+05;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
       ||:|:
Db 1 DDILD 5

RESULT 15
US-11-129-143-170
; Sequence 170, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-11-129-143-170

  Query Match 47.6%; Score 20; DB 7; Length 5;
  Best Local Similarity 60.0%; Pred. No. 1.4e+05;
  Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDLLE 8
       ||:|:
Db 1 DDILD 5

Search completed: April 6, 2006, 16:51:12
Job time : 12.3333 secs